

## SEQUENCE LISTING

01100 University of Utah Research Foundation  
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01200 G-Superfamily Conotoxin Peptides

01300 2314-227

01500 US 60/241,412

01510 2000-10-17

01500 US60/119,440

01510 2000-07-10

01500 US 60 214,263

01510 2000-06-16

01500 US 60 173,754

01510 1999-11-10

01600 400

01700 PatentIn version 3.0

02100 1

02110 101

02120 DNA

02130 *Conus gloriamaris*

02200

02210 CDS

02220 1..1231

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Trp	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Gly	Asn	Gly	Met	Glu	Ile	Leu	
			20					25					30			

tct	cag	aag	ggg	ggg	cac	gaa	atg	gag	aac	ctc	gaa	gtc	tct	aat	cgg	144
Phe	Pro	Lys	Ala	Gly	His	Glu	Met	Glu	Asn	Leu	Glu	Val	Ser	Asn	Arg	
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gtc	aag	cag	tgc	cgt	aaa	gaa	ggg	caa	ctt	tgt	gat	ccg	ata	tta	caa	192
Val	Lys	Pro	Cys	Arg	Lys	Glu	Gly	Gln	Leu	Cys	Asp	Pro	Ile	Phe	Gln	
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aac	tcc	tgc	cgt	ggc	tgg	aat	tgc	gtt	ctt	ttc	tgc	gtc	tgaaactacc	241
Asn	Cys	Cys	Arg	Gly	Trp	Asn	Cys	Val	Leu	Phe	Cys	Val		
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Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu  
 20 25 30

Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg  
 35 40 45

Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln  
 50 55 60

Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val  
 65 70 75

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 <213> Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residue  
 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp  
 or bromo-Trp

<40> 3

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 1 5 10 15

Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val  
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<220>  
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 <223> Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residue  
 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 15 may be Tyr  
 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho  
 6-Tyr; Xaa at residue 22 may be Trp or bromo-Trp

<400> 4

Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Xaa Gln  
1 5 10 15

Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val  
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<223> Xaa at residues 3 and 15 may be pro or hydroxy-Pro; Xaa at residue 8 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp or bromo-Trp; Xaa at residue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, 41-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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1 5 10 15

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tcctcttctt ttgtgtcttg acaga tgg atc agg atg tgc cgt aga gaa gct 172  
Ser Ile Arg Met Cys Arg Arg Glu Ala  
1 5  
caa ctt tgt gtt ccg att ttt caa aac tgc tgc cat ggc ttg ttt tgc 220  
Gln Leu Cys Asp Pro Ile Phe Gln Asn Cys Cys His Gly Leu Phe Cys  
10 15 20 25  
gtt ttg gtc tgc gtc taaaactacc gtgatgtctt ctctccct ctagttagtag 272  
Val Leu Val Cys Val  
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taggggggg ctctagagga tccaagctta cgtacggctg catgagaagt catagctctt 335  
ctatagtgt acctaaattc aattcaactgg ccgtcgtttt acaacgtcgt gaotgggaaa 395  
acccggggtt taccgaactt aatgccttg cagcaccatcc ccccttcgcc agctggcgta 455  
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 <213> Conus omaria

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 20 25 30

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 <217> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residue 11 m  
 ay be Pro or hydroxy-Pro

<400> 8

Met Cys Arg Arg Xaa Ala Gln Leu Cys Asp Xaa Ile Phe Gln Asn Cys  
 1 5 10 15

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 <212> DNA  
 <213> Conus textile

<214>  
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 <216> (15)..(315)

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 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser  
 10 15 20 25

aga aat gga atg gag aat ctt ttt ccg aag gca ggt cac gaa atg gag 147  
 Arg Asn Gly Met Glu Asn Leu Phe Pro Lys Ala Gly His Glu Met Glu  
 30 35 40

aac ctc gaa gac tct aaa cac agg cac cag gag aga ccg gac acc gcc 195  
 Asn Leu Glu Asp Ser Lys His Arg His Glu Glu Arg Pro Asp Thr Gly  
 45 50 55

gac aaa gaa gag atg ctg cta cag aga cag gtc aag ccg tgt cgt aaa 243



Asp Lys Glu Glu Met Leu Leu Gln Arg Gln Val Lys Pro Cys Arg Lys  
60 65 70

gaa cat caa ctt tgt gat ctg att ttt caa aac tgc tgc cgt ggc tgg 291  
Glu His Gln Leu Cys Asp Leu Ile Phe Gln Asn Cys Cys Arg Gly Trp  
75 80 85

tat tgc ctt gtt ctg tct tgc act tgaaagctac ctgatgtgtt ctactcccat 345  
Tyr Cys Val Val Leu Ser Cys Thr  
90 95

c 346

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<212> PRT  
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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Met Glu Asn Leu  
20 25 30

Phe Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Asp Ser Lys His  
35 40 45

Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu  
50 55 60

Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu  
65 70 75 80

Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Val Val Leu Ser Cys  
85 90 95

Thr

<210> 11  
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<212> PRT  
<213> Conus textile

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<222> (1)..(31)  
<223> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residue 4 may be  
Pro or hydroxy-Pro; Xaa at residue 23 may be Trp or bromo-Trp; Xa  
a at residue 24 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr  
, C-sulpho-Tyr or O-phospho-Tyr

<400> 11

Xaa Val Lys Xaa Cys Arg Lys Xaa His Gln Leu Cys Asp Leu Ile Phe  
1 5 10 15

Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Val Val Leu Ser Cys Thr  
20 25 30

<210> 11  
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<212> DNA  
<213> Conus omaria

<220>  
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<222> (1)..(134)

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1 5 10 15

tgg aca ttc gtc acg gct gat gac tct gga aat gga ttg ggg aat ctt 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu  
20 25 30

att tgg aat gaa cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

aac aag aag tgc gtt cca cac gag gcc cct tgt aat tgg ctt aca caa 192  
Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln  
50 55 60

aac tgc tgc aat ggt tat aat tgc atc att ttt ttc tgc cta 234  
Asn Cys Cys Ser Gly Tyr Asn Cys Ile Ile Phe Phe Cys Leu  
65 70 75

taaaataac gtgatgtctt ctcttccct c 265

<210> 12  
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1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu  
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln  
50 55 60

Asn Cys Cys Ser Gly Tyr Asn Cys Ile Ile Phe Phe Cys Leu

65

70

75

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 <223> Xaa at residues 3 and 7 may be Pro or hydroxy-Pro; Xaa at residue  
 5 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Trp  
 or bromo-Trp; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-  
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 14

Cys Val Xaa His Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys  
 1 5 10 15

Ser Gly Xaa Asn Cys Ile Ile Phe Phe Cys Leu  
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<210> 14  
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 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu  
 20 25 30

ttt ccg aag gca cgt cac gaa atg gag aac ctg gaa gac tct aaa cac 144  
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His  
 35 40 45

agg cac bag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192  
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu  
 50 55 60

cag aga bag gtc aag ccg tgt cgt aaa gaa cat caa ctt tgt gat ctg 240  
 Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu  
 65 70 75 80

att ttt caa aac tgc tgc cgt ggc tgg tat tgc ttg ctt cgt cct tgc 288  
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 Ile

<210> 16  
 <211> 97  
 <212> PFT  
 <213> Conus dalli

<400> 16

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Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu  
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His  
 35 40 45

Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu  
 50 55 60

Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu  
 65 70 75 80

Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Leu Leu Arg Pro Cys  
 85 90 95

Ile

<210> 17  
 <211> 31  
 <212> PFT  
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<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 4 and 29  
 may be Pro or hydroxy-Pro; Xaa at residue 8 may be Glu or gamma-  
 carboxy-Glu; Xaa at residue 23 may be Trp or bromo-Trp;

<220>

<221> SITE

<222> (1)..(31)

<223> Xaa at residue 24 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 O-sulpho-Tyr or O-phospho-Tyr

<400> 17

Xaa Val Lys Xaa Cys Arg Lys Xaa His Gln Leu Cys Asp Leu Ile Ile  
 1 5 10 15

Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Leu Leu Arg Xaa Cys Ile  
 20 25 30

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<211> 321  
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 <213> Conus dalli

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 Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu  
 20 25 30  
 ttt cgg aag gca cgt cac gaa atg gag aac ctg gaa gac tct aaa cac 144  
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His  
 35 40 45  
 agg cac cag gag aga cgg gac acg ggc gac aaa gaa gag atg ctg cta 192  
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu  
 50 55 60  
 cag aga cgg gtc aag cgg tgc agt gaa gaa ggt caa ctt tgt gat cca 240  
 Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro  
 65 70 75 80  
 ctt tct caa aac tgc tgc cgt ggc tgg cat tgc gtt ctt gtc tct tgc 288  
 Leu Ser Gln Asn Cys Cys Arg Gly Trp His Cys Val Leu Val Ser Cys  
 85 90 95  
 gtc tgaactacc gtgatgtctt ctctccacc 321  
 Val

<211> 19  
 <212> 37  
 <213> PEST  
 <214> Conus dalli

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 Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu  
 20 25 30  
 Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His  
 35 40 45  
 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu  
 50 55 60  
 Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro  
 65 70 75 80

Leu Ser Gln Asn Cys Cys Arg Gly Trp His Cys Val Leu Val Ser Cys  
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Val

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 <212> FFT  
 <213> Conus dalli

<220>  
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 <222> (1)..(30)  
 <223> Xaa at residues 3 and 13 may be Pro or hydroxy-Pro; Xaa at residues 6 and 7 may be Glu or gamma-carboxy-Glu ; Xaa at residue 22 may be Trp or bromo-Trp

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Asn Lys Cys Arg Gly Xaa His Cys Val Leu Val Ser Cys Val  
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 <213> Conus textile

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 Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly  
                   15                                  20                                  25

ttg ggg aat ctt ttt tgg aat gca cat cac gaa atg aag aac ccc gaa 145  
 Leu Gly Asn Leu Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu  
                   30                                  35                                  40

gcc tct aaa ttg aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt 193  
 Ala Ser Lys Leu Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys  
                   45                                  50                                  55                                  60

aat ttg tta gac caa aac tgc tgc gac ggc tat tgc ata gta ttt gtc 241  
 Asn Leu Leu Asp Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val  
                   65                                  70                                  75

tgc acg taaaactgcc gtgatgtct ctct cccct ctgtgctacc tggcttgatc 297  
 Cys Thr

tttgattggc gegtgtggtt cactgggttat gaaccccccc cccccccccc cccccccccc 357  
 tccggtctct tggaggccctc ggggggttcaa catccaaata aagtgcacag 406

<210> 22  
 <211> 72  
 <212> PRT  
 <213> Conus textile

<400> 22

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
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Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp  
 50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr  
 65 70 75

<210> 13  
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 <212> PRT  
 <213> Conus textile

<210>  
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 <222> (1)..(27)  
 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be  
 Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Tyr,  
 or mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 13

Xaa Cys Lys Gln Asp Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys  
 1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr  
 20 25

<210> 24  
 <211> 27  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be  
 Glu or gamma-carboxy-Glu; Xaa at residue 9 is Nle; Xaa at residue  
 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T

yr or O-phospho-Tyr

&lt;400&gt; 24

Xaa Cys Lys Gln Asp Gly Xaa Xaa Cys Asn Leu Leu Asp Gln Asn Cys  
 5 10 15  
 Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr  
 20 25

&lt;210&gt; 25

&lt;211&gt; 265

&lt;212&gt; DNA

&lt;213&gt; Conus magus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(234)

&lt;400&gt; 25

atg aag atg aag tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
 20 25 30

ttt tgg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192  
 Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp  
 50 55 60

caa aac tgc tgc cac gcc tat tgc ata gta ctt gtc tgc aca 234  
 Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr  
 65 70 75

tataaactgcc gtgatgtctt ctctccct c 265

&lt;210&gt; 26

&lt;211&gt; 28

&lt;212&gt; FRT

&lt;213&gt; Conus magus

&lt;400&gt; 26

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp



50

55

60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr  
65 70 75

<210> 27  
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<220>  
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<222> (1)..(27)  
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be  
Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty  
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 27

Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys  
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr  
20 25

<210> 28  
<211> 27  
<212> PPT  
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<220>  
<221> SITE  
<222> (1)..(27)  
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be  
Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty  
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 23

Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys  
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Phe Val Cys Thr  
20 25

<210> 29  
<211> 265  
<212> DNA  
<213> Conus distans

<220>  
<221> CDS  
<222> (1)..(234)

<400> 29  
atg aaa ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc gcc  
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttt gcc acg gct gat gac ecc aga aat gga ttg ggg aat ctt

48

96

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
 20 25 30  
 ttt tgg aat gca cat cac gaa atg aag aac acc gaa gcc tct aaa ttg 144  
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192  
 Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp  
 50 55 60  
 caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc tgc aca 234  
 Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr  
 65 70 75  
 taaaactgcc gtgatgtctt ctctccct c 265

<210> 30  
 <211> 75  
 <212> PFT  
 <213> Conus distans

<400> 30

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp  
 50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr  
 65 70 75

<210> 31  
 <211> 27  
 <212> FRT  
 <213> Conus distans

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be  
 Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 12-O-Ty  
 1, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 31

Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys  
 1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr

20

25

<210> 32  
 <211> 265  
 <212> DNA  
 <213> *Conus ammiralis*

<220>  
 <221> CDS  
 <222> (1)..(234)

<400> 32  
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
 20 25 30  
 ttt tcc aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac aag agg tgg tgc aaa aaa agc ggt gaa atg tgt aat ttg tta gac 192  
 Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp  
 50 55 60  
 caa aac tgc tgc gag ggc tat tgc ata gta ctt gtc tgc aca 234  
 Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr  
 65 70 75  
 taaaactgcc gtgatgtctt ctctccct c 265

<210> 33  
 <211> 78  
 <212> EST  
 <213> *Conus ammiralis*

<400> 33  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
 20 25 30  
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 Asn Lys Arg Trp Cys Lys Gln Ser Gly Gln Met Cys Asn Leu Leu Asp  
 50 55 60  
 Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr  
 65 70 75

<210> 34  
 <211> 27

<212> PPT  
 <213> Conus ammiralis

<220>  
 <221> SITE  
 <222> (1)..(27)  
 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 7 and 18 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 175-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 34

Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys  
 1 5 10 15  
 Cys Xaa Gly Xaa Cys Ile Val Leu Val Cys Thr  
 20 25

<210> 35  
 <211> 236  
 <212> ENA  
 <213> Conus dalli

<220>  
 <221> CDS  
 <222> (1)..(225)

<400> 35  
 atg aag ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ctt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
 20 25 30  
 ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct aag ttg aat 144  
 Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn  
 35 40 45  
 gag agg tgc ctt ggt ggt ggt gaa gtt tgt gat atc ttt ttt cca caa 192  
 Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln  
 50 55 60  
 tgc tgt ggc tat tgc att ctt ctt ttc tgc aca taaaactacc gtgatgtctt 245  
 Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr  
 65 70 75  
 ctctctccct c 256

<210> 36  
 <211> 75  
 <212> PRT  
 <213> Conus dalli

<400> 36

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn  
35 40 45

Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln  
50 55 60

Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr  
65 70 75

<100> 37  
<110> 25  
<120> PFT  
<130> Genus dalli

<1200>  
<1210> SITE  
<1220> (1) .. (25)  
<1230> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
12 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-  
Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<100> 37

Cys Leu Gly Gly Gly Xaa Val Cys Asp Ile Phe Phe Xaa Gln Cys Cys  
1 5 10 15

Gly Xaa Cys Ile Leu Leu Phe Cys Thr  
20 25

<210> 37  
<211> 441  
<212> DNA  
<213> Genus gloriamaris

<220>  
<221> CDS  
<222> (10) .. (300)

<400> 3:  
gcttgcaag tgaatttggc ttacacagitt tccactgtcg tcttttggcat catctgaaac 60

atcgcaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg 111  
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu  
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 159  
Thr Ala Thr Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly  
15 20 25 30

act att ttt tcg aat gca cat cac gaa atg aag aat ccc gaa gcc tct 207  
Asn Ile Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser  
35 40 45

aaa ttg aac aag agg tgc cgt cta ggg gct gaa agt tgt gat gta att 255  
Lys Leu Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile  
50 55 60

tea caa aac tgc tgc caa ggc acg tgc gtt ttt ttc tgc tta cca 300  
 Ser Gln Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro  
       65                      70                      75

tgatgtcttc tattctcttc tgtgtacct ggttgatct ttcattagcg cgtgcctttc 360  
 actggttaag aacccccctga tccgactctc tggcagcctc ggggggttcaa catccaaata 420  
 aaacgacagc acaatgacaa a 441

<210> 39  
 <211> 77  
 <212> PRT  
 <213> Conus gloriamaris

<400> 39

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
       5                                      10                                      15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Ile  
       20                                      25                                      30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
       35                                      40                                      45

Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile Ser Gln  
       50                                      55                                      60

Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro  
       65                                      70                                      75

<210> 40  
 <211> 26  
 <212> PRT  
 <213> Conus gloriamaris

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
       26 may be Pro or hydroxy-Pro

<400> 40

Cys Arg Leu Gly Ala Xaa Ser Cys Asp Val Ile Ser Gln Lys Cys Cys  
       1                      5                                      10                                      15

Gln Gly Thr Cys Val Phe Phe Cys Leu Xaa  
       20                                      25

<210> 41  
 <211> 446  
 <212> DNA  
 <213> Conus gloriamaris

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (74)..(304)

&lt;400&gt; 41

ggatccttgc acggtgaatt tggcttcaca gttttccast gtcgtctttc gcatcatcca 60

aaacatcacc aag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg 109

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu

1 5 10

ttc ttg acc gcc tgg aca ttc gcc acg gct gat gac ccc aga aat gga 157

Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly

15 20 25

ttg gag aaa ctt ttt tgc aat aca cat cac gaa atg aag aac ccc gaa 205

Leu Glu Lys Leu Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu

10 35 40

gcc tct aaa ttg aac aag agg tgc aaa caa gct gat gaa tct tgt aat 253

Ala Ser Lys Leu Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn

45 50 55 60

gta ttt tca ctt gac tgc tgc acc gcc tta tgc ttg gga ttc tgc gta 301

Val Phe Ser Leu Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val

65 70 75

tcg tgatgtcttc tactccccc tcgtgtacct ggcttgatct ttgattggcg 354

Ser

tgtgcctttc attggttatg aacccccctg atccgattct ttggcgggcct cggggggttca 414

acatccaaaat aaagcgacag cacaataaaaa aa 446

&lt;210&gt; 42

&lt;211&gt; 77

&lt;212&gt; PRF

&lt;213&gt; Conus gloriamaris

&lt;400&gt; 42

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Lys Leu

20 25 30

Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu

35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn Val Phe Ser Leu

50 55 60

Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val Ser

65 70 75

&lt;210&gt; 43

<211> 26  
 <212> PRT  
 <213> Conus gloriamaris

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu.

<400> 45

Cys	Lys	Gln	Ala	Asp	Xaa	Ser	Cys	Asn	Val	Phe	Ser	Leu	Asp	Cys	Cys
1				5				10						15	
Thr	Gly	Leu	Cys	Leu	Gly	Phe	Cys	Val	Ser						
		20						25							

<210> 44  
 <211> 242  
 <212> DNA  
 <213> Conus gloriamaris

<220>  
 <221> CDS  
 <222> (1)..(225)

<400> 44

atg	aaa	ctg	acg	tgc	atg	atg	atc	gtt	gct	gtg	ctg	ttc	ttg	acc	acc	48
Met	Lys	Leu	Thr	Cys	Met	Met	Ile	Val	Ala	Val	Leu	Phe	Leu	Thr	Thr	
1				5				10						15		

tgg	aca	ttc	gcc	acg	gcc	atc	acc	agg	aat	gga	ttg	ggg	aat	ctt	ttt	96
Trp	Thr	Phe	Ala	Thr	Ala	Ile	Thr	Arg	Asn	Gly	Leu	Gly	Asn	Leu	Phe	
			20					25					30			

ccg	aag	aat	cat	cac	gaa	atg	aag	aac	ccc	gaa	gcc	tct	aaa	ttg	aac	144
Pro	Lys	Asn	His	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Leu	Asn	
		35					40					45				

aag	agg	tgc	gtt	cca	tac	gag	ggc	cct	tgt	aat	tgg	ctt	aca	caa	aac	192
Lys	Arg	Cys	Val	Pro	Tyr	Glu	Gly	Pro	Cys	Asn	Trp	Leu	Thr	Gln	Asn	
	50					55					60					

tgc	tgc	gat	gag	cta	tgc	gta	ttt	ttc	tgc	cta	taaaactagc	ctgatgt				242
Cys	Cys	Asp	Glu	Leu	Cys	Val	Phe	Phe	Cys	Leu						
65					70					75						

<210> 45  
 <211> 75  
 <212> PRT  
 <213> Conus gloriamaris

<400> 45

Met	Lys	Leu	Thr	Cys	Met	Met	Ile	Val	Ala	Val	Leu	Phe	Leu	Thr	Thr
1				5				10						15	

Trp	Thr	Phe	Ala	Thr	Ala	Ile	Thr	Arg	Asn	Gly	Leu	Gly	Asn	Leu	Phe
			20					25					30		



Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn  
35 40 45

Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn  
50 55 60

Cys Lys Asp Glu Leu Cys Val Phe Phe Cys Leu  
65 70 75

<210> 46  
<211> 25  
<212> PKT  
<213> Conus gloriamaris

<220>  
<221> SITE  
<222> (1)..(25)  
<223> Xaa at residue 2 and 7 may be Pro or hydroxy-Pro; Xaa at residue  
4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
or O-phospho-Tyr; Xaa at residue 5 and 18 may be Glu or gamma-ca  
rboxy-Glu ; Xaa at residue 10 may be Trp or bromo-Trp

<400> 46

Cys Val Xaa Xaa Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys  
1 5 10 15

Asp Xaa Leu Cys Val Phe Phe Cys Leu  
20 25

<211> 47  
<211> 250  
<212> DNA  
<213> Conus magus

<220>  
<221> CDS  
<222> (1)..(231)

<400> 47

atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctc ttc ttg acc gtc 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val  
1 5 10 15

tgg aca ttc gcc acg gct gat gac tcc gga aat gga ttg gag aaa ctt 96  
Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu  
20 25 30

ttt tgg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

aac aag agg tgc aaa aaa gct gat gaa cct tgt gat gta ttt tca ctt 192  
Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu  
50 55 60

gaa tgc tgc acc gcc ata tgt ctt gga ttc tgc acc tgg tgatgtcttc 241  
Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp  
65 70 75

cctccccctc

250

<210> 43  
 <211> 77  
 <212> PFT  
 <213> Conus magus

&lt;400&gt; 43

Met Lys Leu Thr Cys Val Met Ile Val Ala " " Leu Phe Leu Thr Val  
 1 5 10 15

Trp Tar Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu  
 20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu  
 50 55 60

Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp  
 65 70 75

<210> 49  
 <211> 29  
 <212> PFT  
 <213> Conus magus

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residue 6 and 14 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidue 7 may be Pro or hydroxy-Pro; Xaa at residue 26 may be Trp o  
 r bromo-Trp

&lt;400&gt; 49

Cys Lys Gln Ala Asp Xaa Xaa Cys Asp Val Phe Ser Leu Xaa Cys Cys  
 1 5 10 15

Thr Gly Ile Cys Leu Gly Phe Cys Thr Xaa  
 20 25

<210> 50  
 <211> 434  
 <212> DNA  
 <213> Conus textile

<220>  
 <221> CDS  
 <222> (1)..(295)

<400> 50  
 gctttgcacg gtgaatttgg ctccatagtt ttccactgtc gtctttggca tcatccaaaa 60  
 tcatcccaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 109

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe  
1 5 10

ttg acc gcc tgg aca ttc gcc aag gct gat gac tcc agc aat gga ttg 157  
Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu  
15 20 25

gag aat ctt ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct 205  
Glu Asn Leu Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser  
30 35 40 45

aag ttg aac gag agg tgc ctt gat gct ggt gaa gtt tgt gat att ttt 253  
Lys Leu Asn Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe  
50 55 60

ttt cca aca tgc tgc ggc tat tgc att ctt ctt ttc tgc gca 295  
Phe Pro Thr Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala  
65 70 75

taaaaactacc gtgatgtctt ctactccctt ctgtgtatcc ttggttgatc ttgattggc 355

gggtaccctt tactgggtat gaaacccctg atccagctct ctggaggcct cggggggtca 415

acatccaaat aaagcgaca 434

<210> 51

<211> 75

<212> PRT

<213> Conus textile

<400> 51

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn  
35 40 45

Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe Phe Pro Thr  
50 55 60

Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala  
65 70 75

<210> 52

<211> 25

<212> PRT

<213> Conus textile

<220>

<221> SITE

<222> (1)..(25)

<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

&lt;400&gt; 53

Cys Leu Asp Ala Gly Xaa Val Cys Asp Ile Ile Phe Xaa Thr Cys Cys  
1 5 10 15

Gly Xaa Cys Ile Leu Leu Phe Cys Ala  
20 25

&lt;210&gt; 53

&lt;211&gt; 16

&lt;212&gt; PPT

&lt;213&gt; Conus textile

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(26)

&lt;223&gt; Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at residue 7 may be Pro or hydroxy-Pro

&lt;400&gt; 53

Cys Ile Xaa Gln Phe Asp Xaa Cys Xaa Met Ile Arg His Thr Cys Cys  
1 5 10 15

Val Gly Val Cys Phe Leu Met Ala Cys Ile  
20 25

&lt;210&gt; 53

&lt;211&gt; 16

&lt;212&gt; PPT

&lt;213&gt; Conus textile

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(26)

&lt;223&gt; Xaa at residues 3, 7 and 13 may be Pro or hydroxy-Pro; Xaa at residue 13 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 53

Cys Ala Xaa Phe Leu His Xaa Cys Thr Phe Phe Phe Xaa Asn Cys Cys  
1 5 10 15

Asn Ser Xaa Cys Val Gln Phe Ile Cys Leu  
20 25

&lt;210&gt; 53

&lt;211&gt; 250

&lt;212&gt; DNA

&lt;213&gt; Conus omaria

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(240)

&lt;400&gt; 53

atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc  
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

48

tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ttt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe  
 20 25 30

ttt tgg aag aca caa cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

aac aag agg tgc cta gca gaa cat gaa act tgt aat ata ttt aca caa 192  
 Asn Lys Arg Cys Leu Ala Glu His Glu Thr Cys Asn Ile Phe Thr Gln  
 50 55 60

aac tgc tgc gaa gcc gtg tgc att ttt atc tgc gta caa gct cca gag 240  
 Asn Cys Cys Glu Gly Val Cys Ile Phe Ile Cys Val Gln Ala Pro Glu  
 65 70 75 80

tgatgtcttc tctctccctc 260

<210> 56  
 <211> 80  
 <212> PFT  
 <213> Conus omaria

<400> 56

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe  
 20 25 30

Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Cys Leu Ala Glu His Glu Thr Cys Asn Ile Phe Thr Gln  
 50 55 60

Asn Cys Cys Glu Gly Val Cys Ile Phe Ile Cys Val Gln Ala Pro Glu  
 65 70 75 80

<210> 57  
 <211> 29  
 <212> PFT  
 <213> Conus omaria

<220>

<221> SITE

<222> (1)..(29)

<223> Xaa at residues 4, 6, 17 and 29 may be Glu or gamma-carboxy-Glu;  
 Xaa at residue 28 may be Pro or hydroxy-Pro

<400> 57

Cys Leu Ala Xaa His Xaa Thr Cys Asn Ile Phe Thr Gln Asn Cys Cys  
 1 5 10 15

Xaa Gly Val Cys Ile Phe Ile Cys Val Gln Ala Xaa Xaa  
20 25

<210> 58  
<211> 281  
<212> DNA  
<213> Conus omaria

<220>  
<221> CDS  
<222> (1)..(131)

<400> 58  
arg aaa ctg aat gtc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15  
tgg aca ttt gcc acg gct gaa gac ccc aga cat gga ttg gag aat ctt 96  
Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu  
20 25 30  
ttt tgg aag gca cat cac gaa atg aag aac cct gaa gac tct aaa ttg 144  
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu  
35 40 45  
tac aag agg tcc att cca cat ttt gac cct tgt gac ccc ata gcc cac 192  
Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His  
50 55 60  
acc tgc tgc ttt ggc ctg tgc cta cta ata gcc tgc atc taaaaactgcc 241  
Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile  
65 70 75  
gtgatgtctt ctctcccatc 261

<210> 58  
<211> 77  
<212> PFT  
<213> Conus omaria

<400> 58

Met Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15  
Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu  
20 25 30  
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu  
35 40 45  
Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His  
50 55 60  
Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile  
65 70 75

<210> 60

<211> 26  
 <212> PPT  
 <213> Conus omaria

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.

<400> 60

Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys  
 1 5 10 15  
 Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile  
 20 25

<210> 61  
 <211> 259  
 <212> DNA  
 <213> Conus omaria

<220>  
 <221> CDS  
 <222> (1)..(228)

<400> 61  
 atg aaa ctg aag tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gaa gac ccc aga gat gga ttg aag tat ctt 96  
 Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu  
 20 25 30  
 tta tca aat gca cat aac gaa atg aag aac ccc gaa gcc tct aca ttg 144  
 Leu Ser Asn Ala His Asn Glu Met Lys Asn Pro Glu Ala Ser Thr Leu  
 35 40 45  
 aac gag agg tgc ctt ggg ttt ggt gaa gct tgt ctt ata ctt tat tca 192  
 Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Ile Leu Tyr Ser  
 50 55 60  
 gac tgc tgc ggc tat tgc gtt ggt gct atc tgc cta taaaactacc 238  
 Asp Cys Cys Gly Tyr Cys Val Gly Ala Ile Cys Leu  
 65 70 75  
 gtgatgtctt ctctctccct c 259

<210> 62  
 <211> 76  
 <212> PRT  
 <213> Conus omaria

<400> 62

Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu  
 20 25 30

Leu Ser Asn Ala His Asn Glu Met Lys Asn Pro Glu Ala Ser Thr Leu  
 35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Ile Leu Tyr Ser  
 50 55 60

Asp Cys Cys Gly Tyr Cys Val Gly Ala Ile Cys Leu  
 65 70 75

<210> 63

<211> 21

<212> PRT

<213> Conus omaria

<220>

<221> SITE

<222> (1)..(25)

<223> Xaa at residue m6 ay be Glu or gamma-carboxy-Glu; Xaa at residues  
 12 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s  
 ulpho-Tyr or O-phospho-Tyr

<400> 63

Cys Leu Gly Phe Gly Xaa Ala Cys Leu Ile Leu Xaa Ser Asp Cys Cys  
 1 5 10 15

Gly Xaa Cys Val Gly Ala Ile Cys Leu  
 20 25

<210> 64

<211> 262

<212> DNA

<213> Conus anlicus

<220>

<221> CDS

<222> (1)..(240)

<400> 64

atg aaa ctg acg tgt gtg atg atc gtt got gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttc gcc acg got gat gac ccc aga aat gga ttg gag aat ctt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gln Asn Leu  
 20 25 30

ttt tgg aag aca caa cac aaa atg aag aac ccc gaa gcc ttt aaa ttg 144  
 Phe Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

aaa aaq agg tgc aaa goa gaa aat gaa ctt tgt aat ata ttt ata caa 192  
 Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln  
 50 55 60

aac tgc tgc gac ggg acg tgc ctt ctt atc tgc ata caa aat cca aag 240  
 Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln  
 65 70 75 80



tgatgtcttc tctctaccc tc

262

<210> 65  
 <211> 30  
 <212> PRT  
 <213> Conus aulicus  
 <400> 65

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
 20 25 30

Phe Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln  
 50 55 60

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln  
 65 70 75 80

<210> 66  
 <211> 31  
 <212> PRT  
 <213> Conus aulicus

<220>  
 <221> SITE  
 <222> (1)..(29)  
 <223> Xaa at residues 4 and 6 may be Glu or gamma-carboxy-Glu; Xaa at re-  
 sidue 28 may be Pro or hydroxy-Pro

<400> 66

Cys Lys Ala Xaa Asn Xaa Leu Cys Asn Ile Phe Ile Gln Asn Cys Cys  
 1 5 10 15

Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Xaa Gln  
 20 25

<210> 67  
 <211> 238  
 <212> DNA  
 <213> Conus aulicus

<220>  
 <221> CDS  
 <222> (1)..(228)

<400> 67  
 atg aaa ctg acg tgc gtg atg atc gtt cct atg cta ttc ttg acc gcc  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

48

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gat aat cgt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg  
 20 25 30  
 ttt tgc aag gca cgt cac gaa atg aat aac cgc aga gcc tct aaa ttg 144  
 Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu  
 35 40 45  
 aac aag agg tgc ctt gag ttt ggt gaa ctt tat aat ttt ttt ttc cca 192  
 Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro  
 50 55 60  
 acc tgc tgc ggc tat tgc gtt ctt ctt gtc tgc cta taaactaccg 238  
 Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu  
 65 70 75  
 tgatgtcttc tcttcccttc 258

<210> 68  
 <211> 76  
 <212> PBT  
 <213> Conus aulicus

<400> 68

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg  
 20 25 30

Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro  
 50 55 60

Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu  
 65 70 75

<210> 69  
 <211> 25  
 <212> PBT  
 <213> Conus aulicus

<220>

<221> SITE

<222> (1)..(25)

<223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidue 13 may be Pro or hydroxy-Pro; Xaa at residue 14 may be Tyr  
 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph  
 o-Tyr

<400> 69

Cys Leu Xaa Phe Gly Xaa Leu Cys Asn Phe Phe Phe Xaa Thr Cys Cys

1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu  
20 25

<210> 70

<211> 263

<212> DNA

<213> Conus dalli

<220>

<221> CDS

<222> (1)..(231)

<400> 70

atg aaa atg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttt gtc atg gct gat gac tcc gga aat gga ttg gaa aat ctg 96  
Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu  
20 25 30

ttt tgg aag gca cat cac gaa atg aag aac cct gaa gcc tct aaa ttg 144  
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

aac aag agg tgc gct caa agc agt gaa tta tgt gat gcg ctg gac tca 192  
Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser  
50 55 60

gac tgc tgc agt ggt gtt tgc atg gta ttt ttc tgc cta taaaaatgcc 241  
Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu  
65 70 75

gtgagtctt ctctatcccc tc 263

<210> 71

<211> 77

<212> PRT

<213> Conus dalli

<400> 71

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser  
50 55 60

Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu  
65 70 75

<210> 72  
 <211> 26  
 <212> PRT  
 <213> Conus dalli

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu.

<400> 72

Cys Ala Gln Ser Ser Xaa Leu Cys Asp Ala Leu Asp Ser Asp Cys Cys  
 1 5 10 15  
 Ser Gly Val Cys Met Val Phe Phe Cys Leu  
 20 25

<210> 73  
 <211> 259  
 <212> DNA  
 <213> Conus distans

<220>  
 <221> CDS  
 <222> (1)..(228)

<400> 73  
 atg aag ctg acg tgc gtg atg acc gtt gct gtg atg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gaa gac ccc aga gat gga ttg agg aat ctt 96  
 Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu  
 20 25 30  
 tta tgg aat gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac gag agg tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt tat tca 192  
 Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser  
 50 55 60  
 gac tgc tgc agc tat tgc gtt ggt gct gtc tgc cta taaaactacc 238  
 Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu  
 65 70 75  
 gtgatgtctt ctactcccat c 259

<210> 74  
 <211> 76  
 <212> PRT  
 <213> Conus distans

<400> 74

Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu  
 20 25 30

Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser  
 50 55 60

Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu  
 65 70 75

<210> 75  
 <211> 25  
 <212> PRT  
 <213> Conus distans

<220>  
 <221> SITE  
 <222> (1)..(25)  
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residues  
 12 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s  
 alphi-Tyr or O-phospho-Tyr

<400> 75

Cys Leu Gly Phe Gly Xaa Ala Cys Leu Met Leu Xaa Ser Asp Cys Cys  
 1 5 10 15

Ser Xaa Cys Val Gly Ala Val Cys Leu  
 20 25

<210> 76  
 <211> 262  
 <212> DNA  
 <213> Conus pennaceus

<220>  
 <221> CDS  
 <222> (1)..(231)

<400> 76  
 atg aaa ctg acg tgc ctg atg acc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Leu Met Thr Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttt gcc acg gct gaa gac ccc aga aat gga ttg gag aat ctt 96  
 Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg Asn Gly Leu Glu Asn Leu  
 20 25 30

ttt tgg aag gca cat cac gaa atg aag aac cct gaa gac tct aaa ttg 144  
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu  
 35 40 45

gac aag agg tgc gtt aaa tat ctt gac cct tgt gac atg tta cgc cac 192  
 Asp Lys Arg Cys Val Lys Tyr Leu Asp Pr Cys Asp Met Leu Arg His  
 50 55 60

acc tgc tgc ttt gcc ctg tgc gta cta ata gcc tgc atc taaaaactgcc 241

Thr Cys Cys Phe Gly Leu Cys Val Leu Ile Ala Cys Ile  
65 70 75

gtgatgtatt ctactcccat c

262

<210> 77  
<211> 77  
<212> PRT  
<213> Conus pennaceus

<400> 77

Met Lys Leu Thr Cys Leu Met Thr Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu  
35 40 45

Asp Lys Arg Cys Val Lys Tyr Leu Asp Pro Cys Asp Met Leu Arg His  
50 55 60

Thr Cys Cys Phe Gly Leu Cys Val Leu Ile Ala Cys Ile  
65 70 75

<210> 78  
<211> 26  
<212> PRT  
<213> Conus pennaceus

<220>  
<221> SITE  
<222> (1)..(26)  
<223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or hydroxy-Pro

<400> 78

Cys Val Lys Xaa Leu Asp Xaa Cys Asp Met Leu Arg His Thr Cys Cys  
1 5 10 15

Phe Gly Leu Cys Val Leu Ile Ala Cys Ile  
20 25

<210> 79  
<211> 259  
<212> DNA  
<213> Conus pennaceus

<220>  
<221> CES  
<222> (1)..(228)

<400> 79

atg aaa ctg acg tgt gtg atg atc gtt gct gtg atg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96  
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
20 25 30

ttt tgg aat gca cat cac gaa atg aag aac ccc gaa gct tct aaa ttg 144  
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

aac gag agg tgc ctt ggg ttt ggt gaa gtt tgc aat ttc ttt ttt cca 192  
Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro  
50 55 60

aac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta taaaactacc 238  
Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu  
65 70 75

gtgatgtctt ctattccct c 259

<210> 80  
<211> 76  
<212> PERT  
<213> Conus pennaceus

<400> 80

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro  
50 55 60

Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu  
65 70 75

<210> 81  
<211> 23  
<212> PERT  
<213> Conus pennaceus

<220>  
<221> SITE  
<222> (1)..(25)  
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I  
-Tyr, mono-iodo-Tyr, di-iodo-Ty, O-sulpho-Tyr or O-phospho-Tyr

<400> 81

Cys Leu Gly Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Asn Cys Cys  
 1 5 10 15

Ser Xaa Cys Val Ala Leu Val Cys Leu  
 20 25

<210> 82  
 <211> 260  
 <212> DNA  
 <213> Conus pennaceus

<220>  
 <221> CDS  
 <222> (1)..(240)

<400> 82  
 atg aag ctg acg tgc gtg atg ctc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Leu Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ctc gcc acg gct gat gac tcc agc aat gga ctg gag aat ctt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu  
 20 25 30

ttt tgg aag gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

aac aag agg tgc att cca caa ttt gat cct tgt gac atg gta cgt cac 192  
 Asn Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His  
 50 55 60

act tgc tgc aaa ggg ttg tgc gta cta ata gcc tgc tct aaa act gcg 240  
 Thr Cys Cys Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala  
 65 70 75 80

tgatgtcttctt atctccctctc 260

<210> 83  
 <211> 80  
 <212> PRT  
 <213> Conus pennaceus

<400> 83

Met Lys Leu Thr Cys Val Met Leu Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu  
 20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His  
 50 55 60

Thr Cys Cys Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala



65

70

75

80

<210> 84  
 <211> 29  
 <212> PRT  
 <213> Conus pennaceus

<210>  
 <211> SITE  
 <222> (1)..(29)  
 <223> Xaa at residues 3 and 7 may be Pro or hydroxy-Pro.

<400> 34

Cys Ile Xaa Gln Phe Asp Xaa Cys Asp Met Val Arg His Thr Cys Cys  
 1 5 10 15  
 Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala  
 20 25

<210> 85  
 <211> 260  
 <212> DNA  
 <213> Conus pennaceus

<220>  
 <221> CDS  
 <222> (1)..(240)

<400> 85  
 atg aaa ctg acg tgc ttg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttc ccc acg gct gat gac ccc aga aat gga ttg gag aat ttt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe  
 20 25 30

ttt tgg aag aca caa cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

aac aag agg tgc aaa gca gaa agt gaa gct tgt aat ata att aca caa 192  
 Asn Lys Arg Cys Lys Ala Glu Ser Glu Ala Cys Asn Ile Ile Thr Gln  
 50 55 60

aac tgc tgc gac gcc aag tgc ctt ttt ttc tgc ata caa att cca gag 240  
 Asn Cys Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu  
 65 70 75 80

tgatgtcttc tctcccatc 260

<210> 86  
 <211> 80  
 <212> PRT  
 <213> Conus pennaceus

<400> 86

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe  
 20 25 30

Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Cys Lys Ala Glu Ser Glu Ala Cys Asn Ile Ile Thr Gln  
 50 55 60

Asn Cys Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu  
 65 70 75 80

<210> 87

<211> 29

<212> FET

<213> Conus pennaceus

<220>

<221> SITE

<222> (1)..(29)

<223> Xaa at residues 4, 6 and 29 may be Glu or gamma-carboxy-Glu; Xaa  
 at residue 28 may be Pro or hydroxy-Pro

<400> 87

Cys Lys Ala Xaa Ser Xaa Ala Cys Asn Ile Ile Thr Gln Asn Cys Cys  
 1 5 10 15

Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Xaa Xaa  
 20 25

<210> 88

<211> 632

<212> DNA

<213> Conus omaria

<220>

<221> CDS

<222> (110)..(199)

<400> 88

ggtagacatc atcatcatca tcatccatc tgcacatcca tcatcatt cattcgctgc 60

cagaatgtca taaatattcg agtctctctc tctgtttgta tctgacaga ttg aac aag 135  
 Leu Asn Lys  
 1

agg tgc att gac ggt ggt gaa att tgt gat att ttt ttt cca aac tgc 186  
 Arg Cys Ile Asp Gly Gly Glu Ile Cys Asp Ile Phe Phe Pro Asn Cys  
 5 10 15

tgc agt ggg tgg tgc att att ctc gtc tgc gca tgaactacc gtagatgttt 219  
 Cys Ser Gly Trp Cys Ile Ile Leu Val Cys Ala  
 20 25 30

ctattccct ctagtagtag taggcggcgg ctagtaggga tcaagctta cgtacgggtg 279

catgcgacgt catagctctt ctatagtgtc acctaaattc aattcaactgg ccgtcggttt 339  
 acaacgtcgt gaactgggaaa accctggggt taaccaactt aatcgccctg cagcacatcc 399  
 ccttttcgac agctggcgta atagcgaaga ggcccgccacc gatcgccctt ccaacagttt 459  
 gcgcagcccg aatggcgaat gggacgcgcc ctgtagcggc gcattaagcg cggcgggtgt 519  
 ggtgggtacg cgcagcgtga ccggtacaet tgcacagccc ctacgcgccg ctcccttttc 579  
 tttcttccct tcttttctcg ccaccgttcg cccgggggtt tcccgtaag etc 632

<210> 89  
 <211> 30  
 <212> FRT  
 <213> Conus omaria

<400> 89

Leu Asn Lys Arg Cys Ile Asp Gly Gly Glu Ile Cys Asp Ile Phe Phe  
 1 5 10 15

Pro Asn Cys Cys Ser Gly Trp Cys Ile Ile Leu Val Cys Ala  
 20 25 30

<210> 90  
 <211> 36  
 <212> FRT  
 <213> Conus omaria

<220>  
 <221> SITE  
 <222> 11..(26)  
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or pro-  
 ro-Trp

<400> 90

Cys Ile Asp Gly Gly Xaa Ile Cys Asp Ile Phe Phe Xaa Asn Cys Cys  
 1 5 10 15

Ser Gly Xaa Cys Ile Ile Leu Val Cys Ala  
 20 25

<210> 91  
 <211> 450  
 <212> DNA  
 <213> Conus omaria

<220>  
 <221> CDS  
 <222> (107)..(196)

<400> 91  
 ggtcgacatc atcatcatcg atccatctgt ccacccatcc attcattcat tcgctgccag 60  
 actgtcataa atattcgagt ctctccttct gtttgtatct gacaga ttg aac aag 115  
 Leu Asn Lys  
 1

agg tgc ctt gac ggt ggt gaa att tgt ggt att ttg ttt cca agc tgc 163  
 Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro Ser Cys  
 5 10 15

tgc agt ggg tgg tgc att gtt ctc gtc tgc gca tgaaactacc gtgatgtctt 216  
 Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala  
 20 25 30

ctaactccct ctagtagtag taggcggcgc ctctagagga tccaagctta cgtacgcgtg 276

catgcgaagt catagctctt ctatagtgtc acctaaattc aattcaactgg cgtcgtttt 336

acaacgtcgt gactgggaaa acctggcgt taccctactt aatgccttg cagcacatcc 396

ccctttcgcc agctggcgta atagcgaaga ggccgcacc gatcgccctt cccaacaagt 456

tgcgcagcct gaatggcgaa tgggaacgcgc cctgtacggc cgcattaagc gcggggggtg 516

tggtggttac ggcacacgtg accgtacac ttgccagcgc cctagccgcc cgtcctttc 576

gctttcttcc ctctctttct cgcacgttgc gcggctttc ccgtcaagc tataaatgg 636

gggttccct tttt 650

<210> 92  
 <211> 30  
 <212> FRT  
 <213> Conus omaria

<400> 92

Leu Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe  
 1 5 10 15

Pro Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala  
 20 25 30

<210> 93  
 <211> 24  
 <212> PRT  
 <213> Conus omaria

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro-  
 mo-Trp

<400> 93

Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Ile Xaa Ser Cys Cys  
 1 5 10 15

Ser Gly Xaa Cys Ile Val Leu Val Cys Ala  
 20 25

<210> 94  
 <211> 618

<212> DNA  
 <213> Conus marmoreus

<220>  
 <221> CDS  
 <222> (107)..(193)

<400> 94  
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 actgtaataa atattcgagt ctctctttct gtttgtatct gacaga ttg aac aag 115  
 Leu Asn Lys  
 1  
 agg tgc ctt gag ttt ggt gaa gtt tgt aat ttt ttt ttc cca acc tgc 163  
 Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe Pro Thr Cys  
 5 10 15  
 tgc ggc tat tgc gtt ctt ctt gtc tgc cta taaaactacc gtgatgtctt 213  
 Cys Gly Tyr Cys Val Leu Leu Val Cys Leu  
 20 25  
 ctactccctt ctagtagtag tagggggcgg ctctagagga tccaagetta cgtacggctg 273  
 catggagcgt catagctctt ctatagtgtc acctaaatto aattcactgg ccgtcgtttt 333  
 acaacgtcgt gactgggaaa acctggcgtt taccctactt aatggccttg cagcactcc 393  
 ccccttcgcc agctggcgta atagcgaaga ggcgcgcacc gatcgccctt cccaacagtt 453  
 ggcagcctg aatggcgaat gggacgcgcc ctgtagcggc gcattaagcg cggcggtgt 513  
 ggtggttacg cgcagcgtga ccgtacact tgcagcgccc tagcgccgcg tcccttcgct 573  
 ttctccctt cctttctgc cacttcgcc ggctttcccc gtc aa 618

<210> 95  
 <211> 29  
 <212> PRT  
 <213> Conus marmoreus

<400> 95  
 Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe  
 1 5 10 15

Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu  
 20 25

<210> 96  
 <211> 25  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> SITE  
 <222> (1)..(25)  
 <223> Xaa at residues 3 and 6 may be Ile or gamma-carboxy-Glu; Xaa at residue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 96

Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys  
 1 5 10 15  
 Gly Xaa Cys Val Leu Leu Val Cys Leu  
 20 25

<210> 97  
 <211> 444  
 <212> DNA  
 <213> Conus marmoreus

<220>  
 <221> CDS  
 <222> (150)..(236)

<400> 97  
 gaaagctgggt acgcctgcag gtaccgggtcc ggaattcccg ggtcgacatc atcatcatca 60  
 tggatccatc tgtccatcca tccattcatt cattogetgc cagactgtaa taaatatcg 120  
 ajttctctct tctgtttgta tctgacagg ttg aac aag agg tgc caa gag ttc 173  
 Leu Asn Lys Arg Cys Gln Glu Phe  
 1 5  
 ggt gaa gtt tgt aat ttt ttt ttc cca gac tgc tgc ggc tat tgc gtt 221  
 Gly Glu Val Cys Asn Phe Phe Phe Pro Asp Cys Cys Gly Tyr Cys Val  
 10 15 20  
 ctt tta ctc tgc ata taaaactacc gtgatgtctt ctcttcccat ctagtagtag 276  
 Leu Leu Leu Cys Ile  
 25  
 tagtagtagt aggcgggcgc tctagaggat ccaagcttac gtaagcgtgc atgagacgtc 336  
 atagctcttc tatagtgtca cctaaattca attcactggc cgtcgtttta caacgcgtct 396  
 gactgggaaa acctggcgt tcccaactta attgccttg cagcacaat 444

<210> 98  
 <211> 29  
 <212> PRT  
 <213> Conus marmoreus

&lt;400&gt; 98

Leu Asn Lys Arg Cys Gln Glu Phe Gly Glu Val Cys Asn Phe Phe Phe  
 1 5 10 15  
 Pro Asp Cys Cys Gly Tyr Cys Val Leu Leu Leu Cys Ile  
 20 25

<210> 99  
 <211> 25  
 <212> PRT  
 <213> Conus marmoreus

&lt;220&gt;

<221> SITE  
 <222> 1)..(25)  
 <223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr,  
 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho  
 -Tyr

<400> 99

Cys Gln Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Asp Cys Cys  
 1 5 10 15

Gly Xaa Cys Val Leu Leu Leu Cys Ile  
 20 25

<210> 100  
 <211> 545  
 <212> DNA  
 <213> Conus omaria

<220>  
 <221> CDS  
 <222> (153)..(242)

<223>  
 <221> misc\_feature  
 <222> (1)..(545)  
 <223> n may be any nucleotide

<400> 100  
 ttctgaagcn ggtaagcctg caggtaccgg tccggaatto cggggtcgac atcatcatca 60  
 tcatcgatcc atctgtccat ccattccatto attcattcgc taccagaactg taataaatat 120  
 tccggtctct cttttctgttt gtatctgaca ga ttg gac aag agg tgc att cca 173  
 Leu Asp Lys Arg Cys Ile Pro  
 1 5  
 cat ttt gac cct tgt gac cgg ata cgc cac acc tgc tgc ttt ggc ctg 221  
 His Phe Asp Pro Cys Asp Pro Ile Arg His Thr Cys Cys Phe Gly Leu  
 10 15 20  
 tgc cta cta ata gcc tgc atc taaaaactgcc gtgatgtctt ctctccct 272  
 Cys Leu Leu Ile Ala Cys Ile  
 25 30  
 cta:tagtag tagggggcgg ctctagagga tccaaagetta cgtacggcgtg catgcgaact 332  
 catagctctt ctatagtgtc acctaaatto aattcaactgg ccgtcgtttt acaacgtcgt 392  
 gacggggaaa acctgggggt taccctaaatt aatcggtctg caacacatcc ccttttgcg 452  
 agcggggcta atagcgaaga ggcgcgcacc gatcgacctt cccaacagtt ggcgagcctg 512  
 aatggagaat gggacggcgc ctgtaggggc ggt 545

<210> 101  
 <211> 30  
 <212> PRT  
 <213> Conus omaria

<270>  
 <271> misc\_feature  
 <272> (1)..(545)  
 <273> n may be any nucleotide

<400> 101

Leu Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg  
 1 5 10 15

His Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile  
 20 25 30

<210> 102  
 <211> 26  
 <212> PRT  
 <213> Coccus omaria

<220  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.

<400> 102

Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys  
 1 5 10 15

Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile  
 20 25

<210> 113  
 <211> 34  
 <212> DNA  
 <213> Coccus omaria

<220>  
 <221> CDS  
 <222> (140)..(226)

<400> 103  
 ggtaggcctg caggtaccgg tccggaatto cggggtogag atcatcatca tegatccatc 60

tgtcatcca tccattcttt catttgcgc cagactgtaa taaatattcg agtctctctt 120

tctctttgta tctgacaga ttg aac aag agg tgc ctt gag ttt ggt gaa gtt 172  
 Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val  
 1 5 10

tgt aat ttt ttt ttc cca aac tgc tgc ggc tat tgc gtt ctt ctt gtc 220  
 Cys Asn Phe Phe Phe Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val  
 15 20 25

tgc cta taaaactacc ggtagctctt ctatttcctt ctatgtatg tagggggag 272  
 Cys Leu

ctctagagga tccaagctta cgtacgcgtg catgcgaagt catagctctt ctatagtgtc 336

acctaaatto aattcactgg cgtcgtcttt acaacgtcgt gactgggaaa acctggcgt 396



tacccaactt aatgcgcttg cagcacatcc cccctttgac agcgggogta atagogaaga 456  
 ggccgcacc gatcgccctt cccaacagtt ggcgagctg aatggogaat gggacgcgcc 516  
 ctgttagoggc gcattaag 534

<210> 104  
 <211> 29  
 <212> PRT  
 <213> Conus cmaria

<400> 104

Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe  
 1 5 10 15

Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu  
 20 25

<210> 105  
 <211> 25  
 <212> PRT  
 <213> Conus cmaria

<220>  
 <221> SITE  
 <222> (1)..(25)  
 <223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidue13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr  
 , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph  
 c-Tyr

<400> 105

Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys  
 1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu  
 20 25

<210> 106  
 <211> 200  
 <212> DNA  
 <213> Conus obscurus

<220>  
 <221> CDS  
 <222> (73)..(180)

<400> 106  
 cgtccatct gtccatccat ccattcggtt gttcctgct aaactgtaat aaataacoga 60

gtctctctgt tt gta tct gac aga tct aaa aat gaa tgc att gaa tat ggt 111  
 Val Ser Asp Arg Ser Lys Lys Gln Cys Arg Gln Asn Gly  
 1 5 10

gaa gtg tgt gat gcg aat ttg gca cac tgc tgc agt gac cgg tgt ttt 159  
 Glu Val Cys Asp Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe  
 15 20 25

ctc ttc tgt eta aac cag cag tgatgtcttc tctccctc  
 Leu Phe Cys Leu Asn Gln Pro  
 30 35

<210> 107  
 <211> 36  
 <212> PRT  
 <213> Conus obscurus

<400> 107

Val Ser Asp Arg Ser Lys Lys Gln Cys Arg Gln Asn Gly Glu Val Cys  
 1 5 10 15

Asp Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe Leu Phe Cys  
 20 25 30

Leu Asn Gln Pro  
 35

<210> 108  
 <211> 32  
 <212> PRT  
 <213> Conus obscurus

<220>  
 <221> SITE  
 <222> (1)..(32)  
 <223> Xaa at residue 10 may be Glu or gamma-carboxy-Glu; Xaa at residue  
 s 23 and 32 may be Pro or hydroxy-Pro

<400> 108

Ser Lys Lys Gln Cys Arg Gln Asn Gly Xaa Val Cys Asp Ala Asn Leu  
 1 5 10 15

Ala His Cys Cys Ser Gly Xaa Cys Phe Leu Phe Cys Leu Asn Gln Xaa  
 20 25 30

<210> 109  
 <211> 262  
 <212> DNA  
 <213> Conus ammiralis

<220>  
 <221> CDS  
 <222> (1)..(231)

<400> 109

atg aaa ctg acg tgc gtg atg atc att get gtg ctg ttc ttg acc gcc  
 Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttt gcc acg get gat gac tcc gga aat gga ttg gaa aat ctt  
 Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu  
 20 25 30

ttt tgg aag gca cat cac gaa atg aag aac ccc aaa gcc tct aaa ttg  
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu

48

96

144

25                      40                      45  
 aac aag agg tgc act caa agc ggt gaa ctt tgt gat gtg ata gac cca      192  
 Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro  
   50                      55                      60  
 gac tgc tgc aat aat ttt tgc att ata ttt ttc tgc ata taaaactgcc      241  
 Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile  
   65                      70                      75  
 gtgatgtctt ctaactccct c      262

<210> 110  
 <211> 77  
 <212> PRT  
 <213> Conus ammiralis

<400> 110

Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala  
   1                      5                      10                      15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu  
                     20                      25                      30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu  
                     35                      40                      45

Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro  
   50                      55                      60

Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile  
   65                      70                      75

<210> 111  
 <211> 26  
 <212> PRT  
 <213> Conus ammiralis

<210>  
 <220> SITE  
 <230> (1)..(26)  
 <233> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
           13 may be Pro or hydroxy-Pro

<400> 111

Cys Thr Gln Ser Gly Xaa Leu Cys Asp Val Ile Asp Xaa Asp Cys Cys  
   1                      5                      10                      15

Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile  
                     20                      25

<210> 112  
 <211> 236  
 <212> ENA  
 <213> Conus textile

<220>  
 <221> CIS  
 <222> (25)..(255)

<400> 112 51  
 ggcattacdt aaaacatcac caaa atg aaa ctg acg tgc atg atc gtt  
 Met Lys Leu Thr Cys Met Met Ile Val  
 1 5  
 ggt gtg ctg ttc ttg acc gcc tgg aca ttc gcc acg gct gat gac tcc 99  
 Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Ser  
 10 15 20 25  
 gga aat gga ttg gag aaa ctt ttt tcg aat gca cat cac gaa atg aag 147  
 Gly Asn Gly Leu Glu Lys Leu Phe Ser Asn Ala His His Glu Met Lys  
 30 35 40  
 aac ccc gaa gcc tct aat ttg aac aag agg tgc gct cct ttt ctt cac 195  
 Asn Pro Glu Ala Ser Asn Leu Asn Lys Arg Cys Ala Pro Phe Leu His  
 45 50 55  
 ctt tgt acc ttt ttc ttc cca aac tgc tgc aac gcc tat tgc gtt caa 243  
 Leu Cys Thr Phe Phe Phe Pro Asn Cys Cys Asn Gly Tyr Cys Val Gln  
 60 65 70  
 ttt atc tgc cca taaaactact gtgatgtctt ctattccct c 286  
 Phe Ile Cys Leu  
 75

<210> 113  
 <211> 77  
 <212> PFT  
 <213> Conus textile

<400> 113  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu  
 20 25 30  
 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Asn Leu  
 35 40 45  
 Asn Lys Arg Cys Ala Pro Phe Leu His Leu Cys Thr Phe Phe Phe Pro  
 50 55 60  
 Asn Cys Cys Asn Gly Tyr Cys Val Gln Phe Ile Cys Leu  
 65 70 75

<210> 114  
 <211> 26  
 <212> PRT  
 <213> Conus textile

<220>

<221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residues 3 and 13 may be Pro or hydroxy-Pro; Xaa at residue  
 e 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-  
 Tyr or O-phospho-Tyr

<400> 114

Cys Ala Xaa Phe Leu His Leu Cys Thr Phe Phe Phe Xaa Asn Cys Cys  
 1 5 10 15

Asn Gly Xaa Cys Val Gln Phe Ile Cys Leu  
 20 25

<100> 115  
 <110> 484  
 <120> DNA  
 <130> Conus marmoreus

<220>  
 <221> DMS  
 <222> (74)..(304)

<400> 115  
 ggaatctatgc aagtggaatt tggettcaca gttttccact gtctgtctttg gcatcatcca 60

aaacatcacc aag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg 109  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu  
 1 5 10

ttc atg acc ggc tgg aca ttt gcc acg gct gat gac ccc aga aat gga 157  
 Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly  
 15 20 25

ttg gag aat ctt ttt tgc aag gca cat cac gaa atg aag aac ccc aaa 205  
 Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys  
 30 35 40

gac tct aaa ttg aac aag agg tgc ctt gac gct ggt gaa atg tgt gat 253  
 Asp Ser Lys Leu Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp  
 45 50 55 60

ctt ttt aat tca aaa tgc tgc agt ggg tgg tgc att att ctc ttc tgc 301  
 Leu Phe Asn Ser Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys  
 65 70 75

gca taaaactacc gtgatgtctt ctactccct ctgtgtatcc tggettgate 354  
 Ala

tttgattggc gctgtccctt cactgggttat gaaccccccct gatcagaactc totggggggc 414

tggggggttc aacatccaaa taaagccgac acgatactga cgtagaaaaa aaaaaaaaaa 474

aaaaaaaaaa 484

<110> 116  
 <111> 77  
 <112> PRT  
 <213> Conus marmoreus

<400> 116

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp Leu Phe Asn Ser  
50 55 60

Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys Ala  
65 70 75

<10> 117

<11> 26

<12> PFT

<13> Conus marmoreus

<20>

<21> SITE

<22> (1)..(26)

<23> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
19 may be Trp or bromo-Trp

<40> 117

Cys Leu Asp Ala Gly Xaa Met Cys Asp Leu Phe Asn Ser Lys Cys Cys  
1 5 10 15

Ser Gly Xaa Cys Ile Ile Leu Phe Cys Ala  
20 25

<21> 118

<22> 427

<23> DNA

<24> Conus marmoreus

<221>

<222> CDS

<223> (19)..(249)

<400> 118

gacgaaaaaa tcaccaa'g atg aaa ctg acg agc atg atg atc gtt gct gtg 11  
Met Lys Leu Thr Ser Met Met Ile Val Ala Val  
1 5 10

ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gac gac tcc gga aat 99  
Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn  
15 20 25

gga ttg gag aat ctt ttt tgc aag gca cat cac gag atg aag aac ccc 147  
Gly Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro  
30 35 40

aaa gac tct aaa ttg aac aag agg tgc ctt gac ggt ggt gaa att tgt 195

Lys Asp Ser Lys Leu Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys  
45 50 55

ggt att ttg ttt cca agc tgc tgc agt ggg tgg tgc att gtt ctg gtc 243  
Gly Ile Leu Phe Pro Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val  
60 65 70 75

tgc gca tgaactacc gtgatgtctt ctactccctt ctgtgctacc tggcttgatc 299  
Cys Ala

tttgattggc gcttgccctt cactgggttat gaacccccc gatccgactc tctggcggcc 359

tgggggttc aacatccaaa taaagcgaca cgacaatgac aaaaaaaaaa aaaaaaaaaa 419  
aaaaaaaaa 427

<210> 119

<211> 77

<212> PPT

<213> Conus marmoreus

<400> 119

Met Lys Leu Thr Ser Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro  
50 55 60

Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala  
65 70 75

<110> 130

<111> 24

<112> PPT

<113> Conus marmoreus

<120>

<121> SITE

<122> (1)..(26)

<123> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro  
mo-Trp

<400> 120

Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys  
1 5 10 15

Ser Gly Xaa Cys Ile Val Leu Val Cys Ala

20

25

<110> 121  
 <111> 470  
 <112> DNA  
 <113> *Corvus marmoreus*

<120>  
 <121> CDS  
 <122> (70)..(303)

<400> 111  
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 atccccaag atg aaa ctg acg tgc atg atg atc gaa gca gag ctg ttc ttg 111  
 Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu  
 1 5 10  
 agc aac tgg aca ttt ggc acg gct gat gac ccc aga aat gga ttg gag 159  
 Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu  
 11 20 25 30  
 aat att ttt ttg aag gca cat cac gaa atg aag aac ccc gaa gcc tct 207  
 Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser  
 35 40 45  
 aca ttg aac aag aag tgc cct aac act ggt gaa tta ttt gat gtg gtt 255  
 Lys Leu Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val  
 50 55 60  
 gaa caa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cct ata 303  
 Glu Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile  
 65 70 75  
 ttaactacct gatgtctctt actccccctt gtgtgtgctg gcttgatctt tgattggcgc 363  
 ggcgccttca ctggttatga accccccctga tccgaactctc ttgcggcctc agggggttcaa 423  
 cctccaaaac aagcgacacg aaaatgaaaa aaaaaaaaaa aaaaaaaa 470

<110> 112  
 <111> 75  
 <112> PBT  
 <113> *Corvus marmoreus*

<400> 112

Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
 20 25 30  
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln  
 50 55 60



Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile  
65 70 75

<210> 122  
<211> 27  
<212> PFT  
<213> *Cetus marmoreus*

<220>  
<221> SITE  
<222> (1)..(27)  
<23> Xaa at residues 2 and 26 may be Pro or hydroxy-Pro; Xaa at residues 6 and 12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 123

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys  
1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Xaa Ile  
20 25

<210> 124  
<211> 470  
<212> BHA  
<213> *Cetus marmoreus*

<220>  
<221> CDS  
<222> (1..7)..(312)

<400> 124  
ttggacggg\* g aatttcgctt atatttttct actgtcgtct ttggcatcat ccaaaacatc 60  
accaa g atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg 108  
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu  
1 5 10  
acc acc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta ttg 156  
Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu  
15 20 25 30  
gag aat ttt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc 204  
Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala  
35 40 45  
ttt aaa ttg aac ctg aga gac gac gag tgc gaa cct cct gga gat ttt 252  
Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe  
50 55 60  
tgt ggc ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttc 300  
Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe  
65 70 75  
ctc tgg tgc gcc taaaactgcc gtgatgtctt ctattccct ctgtgctacc 352  
Leu Trp Cys Ala  
80  
tggettgate ttgtattggc gctgcccctt cagtgggttat gaaccccct gatccgaactc 412

tctgggggggccc tcgggggggttc aacatccaaaa taaagctgac aacacaataa aaaaaaaaa

470

<210> 123  
 <211> 82  
 <212> PFT  
 <213> *Conus marmoreus*

<400> 125

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn  
 20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys  
 35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly  
 50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp  
 65 70 75 80

Cys Ala

<210> 126  
 <211> 30  
 <212> PET  
 <213> *Conus marmoreus*

<220>

<221> SITE

<222> (1)...(30)

<223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue  
 s 24 and 28 may be Trp or bromo-Trp

<400> 126

Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile  
 1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala  
 20 25 30

<210> 127  
 <211> 277  
 <212> DNA  
 <213> *Conus striatus*

<220>

<221> CES

<222> (1)...(246)

<400> 127  
 atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gca ttg gag aat 96  
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn  
 20 25 30  
 att tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc tct aaa 144  
 Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys  
 35 40 45  
 atg aac gtg aga gac gac gag tgc gaa cct cct gga gat ttt tgt ggc 192  
 Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly  
 50 55 60  
 tct ttt aaa att ggg cag cct tgc tgc agt ggc tgg tgc ttc ctc tgg 240  
 Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp  
 65 70 75 80  
 tgc gca :aaaaactgcc gtgatgtctt ctctccct c 277  
 Cys Ala

<210> 128  
 <211> 8:  
 <212> PFT  
 <213> Cinus striatus

<400> 128  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn  
 20 25 30  
 Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys  
 35 40 45  
 Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly  
 50 55 60  
 Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp  
 65 70 75 80  
 Cys Ala

<210> 129  
 <211> 8:  
 <212> PFT  
 <213> Cinus striatus

<220>  
 <221> SITE

<222> (1)..(30)

<223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 24 and 25 may be Trp or bromo-Trp

<400> 1-9

Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile  
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala  
20 25 30

<210> 1-0

<211> 277

<212> DNA

<213> *Genus emaria*

<210>

<211> CDS

<212> (1)..(46)

<400> 1-0

atg aaa atg aag tgc gtg atg atc att gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgc aca ttc gtc aag gct gtg cct cac tcc agc aat gca ttg gaa aat 96  
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
20 25 30

ctt tat ctg aag gca cgt cac gaa atg gaa aac ccc gaa gcc tct aaa 144  
Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys  
35 40 45

ctg aac acg aca gac gac gat tgc gaa cct cct gga aat ttt tgt ggc 192  
Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly  
50 55 60

atg ata aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc 240  
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala  
65 70 75 80

tgc gcc taaaaatgcc gtagatgtctt ctctccct c 277  
Cys Ala

<210> 1-1

<211> 37

<212> EMT

<213> *Genus emaria*

<400> 1-1

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys  
 35 40 45

Ile Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly  
 50 55 60

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala  
 65 70 75 80

Cys Ala

<210> 122  
 <211> 30  
 <212> PEST  
 <213> Conus omaria

<220>  
 <221> SITE  
 <222> (1)..(30)  
 <223> Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues  
 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may  
 be Trp or bromo-Trp

<400> 132

Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile  
 1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala  
 20 25 30

<210> 133  
 <211> 277  
 <212> DNA  
 <213> Conus sulicus

<220>  
 <221> CDS  
 <222> (1)..(246)

<400> 133  
 atg aaa ctg acg tcc ctg atg ata gtt gct gtg ctg ttc ttg acg gcc 48  
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gca ttg gag aat 46  
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
 20 25 30

ctt tat ctg aag gca cgt cac gaa atg gaa aac ccc gaa gcc tct aag 144  
 Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys  
 35 40 45

ttg aac acg aga gac tac gat tgc gaa cct cct gga aat ttt tgt gcc 192  
 Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly  
 50 55 60

atg ata aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc 240

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala  
 65 70 75 80

acc gcc taaaactgcc gtgatgtatt ctctctccct c  
 Cys Ala

277

<110> 134  
 <111> 82  
 <112> PFT  
 <113> Conus aulicus

<400> 134

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
 20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys  
 35 40 45

Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly  
 50 55 60

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala  
 65 70 75 80

Cys Ala

<110> 135  
 <111> 30  
 <112> PFT  
 <113> Conus aulicus

<220>  
 <221> SITE  
 <222> (1..30)  
 <223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 may be Glu or  
 gamma-carboxy-Glu; Xaa at residues 6, 7, 13 and 19 may be Pro or  
 hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

<400> 135

Asp Xaa Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile  
 1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala  
 20 25 30

<210> 136  
 <211> 635  
 <212> DNA

<215> Conus marmoreus

<220>

<221> CDS

<222> (111)..(212)

<400> 136

ggtgacatc atcatcatca tcatccatc tgtcatcca tctattcatt cattcgtggc 60

caantgttaa taaataatgc aagtctctct tctgttttgt atctgacaga ttg aac 116  
Leu Asn  
1

agc aga gac gac gat tgc gaa cct cct gga aat ttt tgt ggc atg ata 164  
Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly Met Ile  
5 10 15

aaa att agg cgg cct tgc tgc agt ggc tgg tgc ttt ttc gcc tgc gcc 212  
Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala Cys Ala  
20 25 30

taaaactgac gtgatgtctt ctcttccctt ctagttagtag tagggggcgg ctctagagga 272

cccaagctta cgtacggctg catgcgacgt catagctctt ctatagtgtc acctaaattc 332

aaactactgg cgtcgtttt acaacgtcgt gaactgggaaa accttggcgt taccctaaatt 392

aatcccttgg cagcacatcc ccttttcgcc agctggcgta atagcgaaga ggcctgcacc 452

gaccccttcc cccaacagtt ggcgacgtg aatggcgaat gggacgcgcc ctgtagcggc 512

gcattaaagg cggcgggtgt ggtgggttac cgcgacgtg gacccgtctac acttgccagc 572

gccttagcgc cgtctctttt cgttttcttc ctctcttctt cgcacagttc gcgggtttt 632

ccgtcaagg cctaaatcgg gggtctcttt aggttcctat ttaagtgtt tac 685

<215> 137

<215> 34

<215> PFT

<215> Conus marmoreus

<400> 137

Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly  
1 5 10 15

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala  
20 25 30

Cys Ala

<215> 138

<215> 31

<215> PFT

<215> Conus marmoreus

<220>

<221> SITE

<222> (1)..(30)  
 <223> Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 13 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

<400> 173

Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile  
 1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala  
 20 25 30

<210> 139

<211> 1.6

<212> DNA

<213> *Canus regius*

<210>

<211> 318

<212> (1)..(96)

<400> 179

ttg aac tag aga gac tgc ctt agt aaa aac gct ttc tgt gcc tgg ccg 48  
 Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro  
 1 5 10 15

ata ctt aga gaa ctg tgc tgc agt ggc tgg tgc tta tac gtc tgc atg 96  
 Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met  
 20 25 30

taaaactgac g'gatgtctt ctatccctc 126

<210> 140

<211> 31

<212> PPT

<213> *Canus regius*

<400> 140

Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro  
 1 5 10 15

Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met  
 20 25 30

<210> 141

<211> 31

<212> PPT

<213> *Canus regius*

<220>

<221> SITE

<222> (1)..(23)

<223> Xaa at residues 11 and 22 may be Trp or bromo-Trp; Xaa at residue 12 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tyr, 1:5-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr



&lt;400&gt; 141

Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa  
 1 5 10 15

Leu Cys Cys Ser Gly Xaa Cys Leu Xaa Val Cys Met  
 20 25

&lt;210&gt; 142

&lt;211&gt; 123

&lt;212&gt; DNA

<213> *Citrus radiatus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; ( )..(103)

&lt;400&gt; 142

1 ttt aac aag aaa ggt gat gac tgc ctt gct gtt aaa aaa aat tgt ggc 49  
 Leu Asn Lys Lys Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly  
 1 5 10 15

ttt aca aaa ctt gga ggg cca tgc tgc agt ggc ttg tgc ttt ttc gtc 97  
 Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val  
 20 25 30

tgc gcc taaaaactgcc gtgatgtctt ctctccctt 133  
 Cys Ala

&lt;210&gt; 143

&lt;211&gt; 34

&lt;212&gt; PPT

<213> *Citrus radiatus*

&lt;400&gt; 143

Leu Asn Lys Lys Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly  
 1 5 10 15

Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val  
 20 25 30

Cys Ala

&lt;210&gt; 144

&lt;211&gt; 35

&lt;212&gt; PPT

<213> *Citrus radiatus*

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; ( )..(30)

&lt;223&gt; Xaa at residues 14 and 19 may be Pro or hydroxy-Pro.

&lt;400&gt; 144

Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly Phe Xaa Lys Leu

1                    5                    10                    15  
 Gly Gly Xaa Cys Cys Ser Gly Leu Cys Phe Phe Val Cys Ala  
                   20                    25                    30

<210> 145  
 <211> 127  
 <212> DNA  
 <213> Conus regius

<220>  
 <221> CDS  
 <222> (1)..(96)

<400> 145  
 tgg aat cag agc gac tgc ctt cct aga gac aca ttc tgt gcc ttg ccg                    48  
 Leu Asn Gln Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro  
                   5                    10                    15

aaa ctt gga cta ctg tgc tgc agt ggc cgg tgc tta ctc ttc tgc gtg                    96  
 Gln Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val  
                   20                    25                    30

taaaaactgac gtgatgtatt ctactccact c                    127

<410> 146  
 <411> 81  
 <412> PBT  
 <413> Conus regius

<420> 116  
 Leu Asn Gln Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro  
                   5                    10                    15

Gln Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val  
                   20                    25                    30

<430> 147  
 <431> 28  
 <432> PBT  
 <433> Conus regius

<440>  
 <441> SITE  
 <442> (1)..(25)  
 <443> Xaa at residues 4 and 12 may be Pro or hydroxy-Pro.

<450> 147  
 Asp Cys Leu Xaa Arg Asp Thr Phe Cys Ala Leu Xaa Gln Leu Gly Leu  
                   5                    10                    15

Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val  
                   20                    25

<210> 148  
 <211> 345  
 <212> DNA  
 <213> Conus aurisiacus

<222> (1) .. (234)

atg aaa ctg acg tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aga ttc gtc acg gct gat gac tcc aga aat gga ctg aag aat ctt      96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu  
                30                         28                         30

ttt tgg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

aac arg arg gat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192  
Asn Lys Arg Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His  
50 55 60

cca tga ctc tgc tgc agc gag att tgc att gtt tgg tgc aca 234  
Pro Gly Leu Cys Cys Ser Glu Ile Cys Ile Val Trp Cys Thr  
65 75

tgagtcgtat: tatgctggta cattttgtgg attcaacgga ggactctgct gcagcaacct 294

ttggttatt: ttggtgtgc: taacatattc gtgatgtctt ctactcccat c 345

Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu  
20 25 30

The Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His  
50 55 60

Pro Gly Leu Cys Cys Ser Glu Ile Cys Ile Val Trp Cys Thr  
65 70 75

 $\langle 220 \rangle$

&lt;221&gt; SITE

&lt;222&gt; (1)..(27)

<223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

&lt;400&gt; 15

Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Ile Cys Ile Val Xaa Cys Thr  
20 25

&lt;210&gt; 151

&lt;211&gt; 412

&lt;212&gt; DNA

<213> *Coccus purpurascens*

&lt;210&gt;

&lt;211&gt; CDS

&lt;212&gt; (1)..(243)

&lt;400&gt; 151

Met Ala Cys Arg Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15 48

Arg Ala Thr Cys Arg Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
20 25 30 96

Met Ala Cys Arg Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
35 40 45 144

Met Ala Cys Arg Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
50 55 60 192

Met Ala Cys Arg Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
65 70 75 80 240

Met Ala Cys Arg Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
85 90 95 100 293

Met Ala Cys Arg Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
105 110 115 120 353

Met Ala Cys Arg Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
125 130 135 140 412

&lt;210&gt; 152

&lt;211&gt; 31

&lt;212&gt; PRT

<213> *Coccus purpurascens*

&lt;400&gt; 152

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys  
50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly  
65 70 75 80

Gly

(2100) 153  
(2110) 24  
(2120) PRT  
(2130) *Cinus purpurascens*

(2200)  
(2210) SITE  
(2220) (1) .. (29)  
(2230) Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

(3100) 155

Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly  
20 25

(3210) 156  
(3211) 24  
(3212) PRT  
(3213) *Cinus purpurascens*

(3300)  
(3310) SITE  
(3320) (1) .. (29)  
(3330) Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

(4000) 154

Xaa Ala Cys Xaa Ala Xaa Gly Thr Ala Cys Gly Ile Lys Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly  
20 25

<210> 155  
 <211> 19  
 <212> PBT  
 <213> *Canis purpurascens*

<214>  
 <215> SITE  
 <216> (1)..(29)  
 <217> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 155

Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ala Lys Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly  
 20 25

<210> 155  
 <211> 19  
 <212> PBT  
 <213> *Canis purpurascens*

<214>  
 <215> SITE  
 <216> (1)..(29)  
 <217> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 155

Xaa Ala Cys Xaa Ala Xaa Gly Ala Phe Cys Gly Ile Lys Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly  
 20 25

<210> 157  
 <211> 159  
 <212> DNA  
 <213> *Canis lupus*

<220>  
 <221> IDS  
 <222> (1)..(252)

<400> 157  
 atg aaa ctg acg tgc gtg atg atc gtt gct gtc ctg ttc ttg acc acc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
 20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg 144

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
           35                          40                          45  
 aac aag aga gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt       192  
 Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg  
           50                          55                          60  
 aca gga ctc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt       240  
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
           55                          70                          75                          80  
 gtt gat tct ggc taacagtgtg cgttggttag tgcctctcc tcccttc       289  
 Val Asp Ser Gly

<210> 153  
 <211> 84  
 <212> PRT  
 <213> Conus magus

<400> 153

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
           5                          10                          15  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
           20                          25                          30  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
           35                          40                          45  
 Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg  
           50                          55                          60  
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
           65                          70                          75                          80  
 Val Asp Ser Gly

<210> 153  
 <211> 82  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> SITE  
 <222> (1)...(32)  
 <223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or  
 hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;  
 Xaa at residue 25 may be Trp or bromo-Trp

<400> 153

Asp Gly Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu

1                      5                      10                      15  
 Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser  
                     20                      25                      30

<210> 100  
 <211> 273  
 <212> DNA  
 <213> Conus magus

<220>  
 <221> CDS  
 <222> (1)..(249)

<230> 100  
 atg aaa ctg aag tgc gtg atg atc gtt get gtg ctg ttc ttg acc acc 43  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
                     5                      10                      15

tgg gga ttc gtc aag gct gat gac tcc aga tat gga ttg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
                     20                      25                      30

ttt aag aag gga cgt cat gaa atg aag aac cct gaa ggc tat aaa ttg 144  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
                     35                      40                      45

aac aag aga gat gaa tgc tat cct cct ggt aca ttt tgt ggc atc aaa 192  
 Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
                     50                      55                      60

cca gga ctt tgc tgc agc ggc ata tgc tta tog ttt gtc tgc ata tca 240  
 Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser  
                     65                      70                      75                      80

tat gat ttt tcatgatgt cttctcctcc cctc 273  
 Phe Asp Phe

<210> 101  
 <211> 83  
 <212> PRT  
 <213> Conus magus

<2400> 101

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
                     5                      10                      15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
                     20                      25                      30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
                     35                      40                      45

Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
                     50                      55                      60

Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser



65

70

75

80

Phe Asp Phe

4210+ 162

4211+ 3.

4212+ PKT

4213+ Conus magus

4220+

4221+ SITE

4222+ 11... (32)

4223+ Xaa at residue 2 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6 and 14 may be Pro or hydroxy-Pro

4400+ 162

Asp Xaa Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
 1 5 10 15

Tyr Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe  
 20 25 30

4410+ 162

4411+ 254

4412+ PCA

4413+ Conus magus

4420+

4421+ CDS

4422+ (1... (252)

4400+ 162

atc aaa atg acg tgc gtg atg atc gtt gct gta ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgc aca ttc gtc acg gct gat gac tcc aga tat gga ctg aag gat ctg 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu  
 20 25 30

ttt aag aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

aac aag aca gaa gcc tgc tat aat gct ggt tca ttt tgt ggc atc cat 192  
 Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Ser Phe Cys Gly Ile His  
 50 55 60

aca aga ctc tgc tgc acc gag ttt tgc att att tgg tgc ata aca ttt 240  
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Ile Leu Trp Cys Ile Thr Phe  
 65 70 75 80

gtt gat tct ggc taaatgtgtg cgttgggttga tgtcttctcc tcccatc 289  
 Val Asp Ser Gly

<210> 164  
 <211> 84  
 <212> PRT  
 <213> Conus magus

<400> 164

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu  
 20 25 30

Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Ser Phe Cys Gly Ile His  
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Ile Leu Trp Cys Ile Thr Phe  
 65 70 75 80

Val Asp Ser Gly

<210> 165  
 <211> 3  
 <212> PPT  
 <213> Conus magus

<220>  
 <221> SITE  
 <222> (1)...(32)  
 <223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at  
 residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su  
 lpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydrox  
 y-Pro; Xaa at residue 25 may be Trp or bromo-Trp

<400> 165

Xaa Ala Cys Xaa Asn Ala Gly Ser Phe Cys Gly Ile His Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Ile Leu Xaa Cys Ile Thr Phe Val Asp Ser  
 20 25 30

<210> 166  
 <211> 271  
 <212> DNA  
 <213> Conus magus

<221>  
 <222> CDS  
 <223> (1)...(249)

<400> 166  
 atg aaa ctg acg tgc atg atg atc gtt gct gta ctg ttc ttg acc gcc

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ctg aag gat ctg 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu  
20 25 30

ttt ccg aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

aac cag aga gaa gcc tgc tat aat gct ggt aca ttt tgt ggc atc aaa 192  
Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys  
50 55 60

cba gga ctt tgc tgc agc gcg ata tgc tta tcc ttt gtc tgc ata tca 240  
Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser  
65 70 75 80

ttt gat ttg attgaagtct tctctccccc tc 271  
Phe Asp Leu

<210> 16''

<211> 83

<212> PRT

<213> Conus magus

<400> 16''

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu  
20 25 30

Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys  
50 55 60

Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser  
65 70 75 80

Phe Asp Leu

<210> 166

<211> 32

<212> PRT

<213> Conus magus

<220>

<221> SITE

<222> (1)..(32)

<223> Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residue

4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro

<400> 168

Xaa Ala Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
1 5 10 15

Cys Lys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe  
20 25 30

<210> 168

<211> 277

<212> DNA

<213> *Conus ermineus*

<220>

<221> CDS

<222> (1..(243)

<400> 168

atg aag ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgc aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144  
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192  
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
50 55 60

ccc ggg cca tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240  
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly  
65 70 75 80

ggt taactgccgt gatgtcttct cctccctc 272  
Gly

<210> 170

<211> 81

<212> PFT

<213> *Conus ermineus*

<400> 170

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly  
65 70 75 80

Gly

02100 171  
02110 29  
02120 PRT  
02130 Conus ermineus

02140  
02150 SITE  
02160 (1...119)  
02170 Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at  
residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su  
lpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be  
Pro or hydroxy-Pro

04000 171

Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly  
20 25

02100 172  
02110 173  
02120 DNA  
02130 Conus purpurascens

02140  
02150 CDS  
02160 (1...143)

04000 172

atg aag atg aag tgc atg atg atc gtt gct gtg atg ttc ttg act gcc 48  
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttc atc aag gct gat gac tcc aaa aat gga atg gag aat cat 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

ttt tgg aag gta cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144  
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

gac aag aag gaa gcc tgc tat ccg cct ggt aat ttt tgt ggc ata aag 192  
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
50 55 60

ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240  
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly

65

70

75

80

ggt taactgcogt gatgtcttct cctccctc  
Gly

272

&lt;210&gt; 173

&lt;211&gt; 31

&lt;212&gt; PFT

&lt;213&gt; Conus purpurascens

&lt;400&gt; 173

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly  
65 70 75 80

Gly

&lt;210&gt; 174

&lt;211&gt; 23

&lt;212&gt; PFT

&lt;213&gt; Conus purpurascens

&lt;210&gt;

&lt;211&gt; SITE

&lt;222&gt; (1)..(29)

<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at  
residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su  
lpho-Tyr or C-phospho-Tyr; Xaa at residues 14 and 24 may be Pro o  
r hydroxy-Pro

&lt;400&gt; 174

Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly  
20 25

&lt;210&gt; 175

&lt;211&gt; 206

&lt;212&gt; DNA

&lt;213&gt; Conus striatus

<220>  
 <221> CDS  
 <222> (1)..(246)

<400> 175  
 atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc aat 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
 1 5 10 15  
 tgg aca ttc gtc aag gct gat gac tcc aga tat gga ttg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
 20 25 30  
 ttt cag aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac aag aga gaa ggg tgc tct agt gct ggt aca ttt tgt ggc atc cat 192  
 Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His  
 50 55 60  
 cca gga ctg tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240  
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
 65 70 75 80  
 att cat tgaatgtcttc tctctccctc 266  
 Ile Asp

<210> 176  
 <211> 82  
 <212> PPT  
 <213> *Corvus striatus*

<400> 176  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr  
 1 5 10 15  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
 20 25 30  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His  
 50 55 60  
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
 65 70 75 80  
 Ile Asp

<210> 177  
 <211> 31

<212> PPT  
<213> *Conus striatus*

<220>  
<221> SITE  
<222> (1)...(31)  
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or bromo-Trp

<400> 177

Xaa	Gly	Cys	Ser	Ser	Gly	Gly	Thr	Phe	Cys	Gly	Ile	His	Xaa	Gly	Leu
1				5					10					15	
Cys	Cys	Ser	Xaa	Phe	Cys	Phe	Leu	Xaa	Cys	Ile	Thr	Phe	Ile	Asp	
			20					25					30		

<210> 178  
<211> 266  
<212> DNA  
<213> *Conus striatus*

<220>  
<221> CDS  
<222> (1)...(246)

<400> 178

atg	aaa	tgg	acg	tgc	gtg	atg	atc	ggt	gct	gtg	ctg	ttc	tgg	acc	act	48
Met	Lys	Leu	Thr	Cys	Val	Met	Ile	Val	Ala	Val	Leu	Phe	Leu	Thr	Thr	
1				5				10					15			
tgg	aca	ttc	gtc	acg	gct	gat	gac	tcc	aga	tat	gga	tgg	aag	cat	ctt	96
Trp	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Tyr	Gly	Leu	Lys	Asn	Leu	
			20					25					30			
ttc	acg	aag	aca	ggt	cat	gaa	atg	aag	aac	ccc	gaa	gcc	tct	aaa	tgg	144
Phe	Pro	Lys	Ala	Arg	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Leu	
		35					40					45				
aac	aag	aga	gat	ggg	tgc	tct	agt	ggt	ggt	aca	ttt	tgt	ggc	atc	cat	192
Asn	Lys	Arg	Asp	Gly	Cys	Ser	Ser	Gly	Gly	Thr	Phe	Cys	Gly	Ile	His	
	50					55				60						
cca	tga	ccc	tgc	tgc	agc	gag	ttt	tgc	ttt	ctt	tgg	tgc	ata	aca	ttt	240
Pro	Gly	Leu	Cys	Cys	Ser	Glu	Phe	Cys	Phe	Leu	Trp	Cys	Ile	Thr	Phe	
65				70				75					80			
att	gat	tgatgtcttc	tctctccctc													266
Ile	Asp															

<210> 179  
<211> 80  
<212> PPT  
<213> *Conus striatus*

<400> 179

Met	Lys	Leu	Thr	Cys	Val	Met	Ile	Val	Ala	Val	Leu	Phe	Leu	Thr	Thr
1				5				10					15		



Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
                   20                  25                  30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
           35                  40                  45

Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His  
       50                  55                  60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
       65                  70                  75                  80

Ile Asp

<210> 180

<211> 31

<212> P5T

<213> *Conus striatus*

<220>

<221> SITE

<222> (1...31)

<223> Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue  
       14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or br  
       omo-Trp

<400> 180

Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His Xaa Gly Leu  
       1                  5                  10                  15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp  
           20                  25                  30

<210> 181

<211> 31

<212> P5T

<213> *Conus striolatus*

<220>

<221> SITE

<222> (1...31)

<223> Xaa at residues 6 and 14 may be Pro or hydroxy-Pro; Xaa at residu  
       e 11 may be Glu or gamma-carboxy-Glu

<400> 181

Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
       1                  5                  10                  15

Cys Cys Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa  
           20                  25                  30

<210> 182

<211> 345

<212> DNA  
 <213> Conus catus

<220>  
 <221> CDS  
 <222> (1)..(234)

<400> 132  
 atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gat gac tcc aga aat gga ctg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu  
 20 25 30  
 ttt acg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac aag aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192  
 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His  
 50 55 60  
 cca gga ctc tgc tgc agc gag ctt tgc ctg gtt tgg tgc aca 234  
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr  
 65 70 75  
 tgagtgctat tcttcggta cattttgtgg ctccaacgga ggactctgct gcagcaacct 294  
 ttgcatttt tctgtgtgctt aacatttctg gatgtcttct ctattccct c 345

<210> 183  
 <211> 7:  
 <212> P&T  
 <213> Conus catus

<400> 183  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu  
 20 25 30  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His  
 50 55 60  
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr  
 65 70 75

<210> 184  
 <211> 27  
 <212> P&T  
 <213> Conus catus

0020>  
 0021> SITE  
 0022> (1)..(27)  
 0023> Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or  
 hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;  
 Xaa at residue 25 may be Trp or bromo-Trp

0400> 184

Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu  
 1 5 10 15  
 Cys Cys Ser Xaa Leu Cys Leu Val Xaa Cys Thr  
 20 25

00100> 185

00110> 345

00120> DNA

00130> Conus catus

00200>

00210> CDS

00220> (1)..(34)

0400> 185

Arg aaa ctg aag tgt arg atg atc gtt gct ggg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Arg aca ttc gtc aag gct gat gac tcc aga tat gga ctg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
 20 25 30

ttt aag aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

aac aag aga tat ggg tgc tct aat gct ggt gaa ttt tgt ggc atc cat 192  
 Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His  
 50 55 60

gaa gga ctg tgc tgc agc gag ctt tgc atg ggt tgg tgc aca 234  
 Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr  
 65 70 75

taagtgctat tctactggta cattttgtgg ctccaacgga ggactctgct gcagcaacct 294

tggctatatt tgggtgtgctt aacatttctg gatgkcttct ctattccct c 345

00100> 186

00110> 78

00120> PRT

00130> Conus catus

0400> 186

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
20 25 30

Ile Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His  
50 55 60

Phe Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr  
65 70 75

110 187

111 27

112 PPT

113 Conus catus

120

121 SITE

122 1... (17)

123 Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or Bromo-Trp

140 187

Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu  
1 5 10 15

Lys Cys Ser Xaa Leu Cys Leu Gly Xaa Cys Thr  
20 25

110 188

111 246

112 CNA

113 Conus distans

121

121 SITE

122 1... (246)

140 188

atg aaa atg acg tgt ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

atg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctc 96  
Trp Thr Ile Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
20 25 30

atg aag aag gca cct cac gaa atg aag aac ccc gaa gcc tct aaa tgg 144  
Ser Pro Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser  
35 40 45

aac aac aga tat gag tgc tat c. ctc gta tat ttt tgt ggc atc aac 192  
Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn  
50 55 60

gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240  
 Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr  
 65 70 75 80

ttc tgg tga tgc ttc tctcccatc 266  
 Phe Ser

<210> 189  
 <211> 82  
 <212> PFT  
 <213> Conus distans

<400> 189

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
 20 25 30

Ser Pro Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser  
 35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn  
 50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr  
 65 70 75 80

Phe Ser

<210> 190  
 <211> 31  
 <212> PFT  
 <213> Conus distans

<220>  
 <221> SITE  
 <222> (1...31)  
 <223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, ci-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be  
 Glu or gamma-carboxy-Glu

<400> 190

Xaa Xaa Cys Xaa Leu Leu Val His Phe Cys Gly Ile Asn Gly Gly Leu  
 1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser  
 20 25 30

<210> 191  
 <211> 113  
 <212> DNA

<113> Conus regius

<120>

<121> CDS

<122> (1)..(93)

<400> 191

ttg agc aag aga gac tgc ctt cct gac tac acg att tgt ggc ttc aat 48  
Leu Ser Lys Arg Asp Cys Leu Pro Asp Tyr Thr Ile Cys Ala Phe Asn  
1 5 10 15

atg cgt ctg tgc tgc agc gac aag tgc atg ctg gtc tgc ctg ccg 93  
Met Gly Leu Cys Cys Ser Asp Lys Cys Met Leu Val Cys Leu Pro  
20 25 30

aga gctcttc tcttccctc 113

<110> 191

<111> 31

<112> PFT

<113> Conus regius

<400> 192

Leu Ser Lys Arg Asp Cys Leu Pro Asp Tyr Thr Ile Cys Ala Phe Asn  
1 5 10 15

Met Gly Leu Cys Cys Ser Asp Lys Cys Met Leu Val Cys Leu Pro  
20 25 30

<111> 193

<111> 17

<112> PFT

<113> Conus regius

<120>

<121> SITE

<122> (1)..(17)

<123> Xaa at residues 5 and 27 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 192

Asp Cys Leu Xaa Asp Xaa Thr Ile Cys Ala Phe Asn Met Gly Leu Cys  
1 5 10 15

Cys Ser Asp Lys Cys Met Leu Val Cys Leu Xaa  
20 25

<110> 194

<111> 116

<112> DNA

<113> Conus regius

<120>

<121> CDS

<122> (1)..(96)

<400> 194

ttg aac aag aga atc atc tgc ttt cct gac tac atg ttt tgt ggc gtc 48  
 Leu Asn Lys Arg Ile Ile Cys Phe Pro Asp Tyr Met Phe Cys Gly Val  
 1 5 10 15

aat arg ttt ctg tgc tgc agt ggc aac tgc ctt ctc atc tgc gtg cag 96  
 Asn Val Phe Leu Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Pro  
 20 25 30

tgatgtcttc taactccctc 116

110 195  
 111 32  
 112 FFT  
 113 Conus regius

1400 195

Leu Asn Lys Arg Ile Ile Cys Phe Pro Asp Tyr Met Phe Cys Gly Val  
 1 5 10 15

Asn Val Phe Leu Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Pro  
 20 25 30

11 186  
 111 24  
 111 FFT  
 111 Conus regius

12  
 121 SITE  
 122 (1) (11)  
 123 Xaa at residues 5 and 28 may be Pro or hydroxy-Pro; Xaa at residue  
 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr

1410 196

Ile Ile Cys Gly Xaa Asp Xaa Met Phe Cys Gly Val Asn Val Phe Leu  
 1 5 10 15

Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Xaa  
 20 25

11 187  
 111 219  
 111 DNA  
 111 Conus gloriamaris

11  
 111 CDS  
 11 (1) (128)

14 197  
 ttc aac atg aag tgc atg atg atc gtt gct atg atg ttc ttg acc gcc 48  
 Met Cys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tga aca ttc gtc acg gct atg cct cac tcc agc aat gcg ttg gag aat 96  
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
 20 25 30

ctt tat ctg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa 144  
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu  
 35 40 45  
 ttg aac aag agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac 192  
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn  
 50 55 60  
 caa tgc tgc agt ggc tgg tgc att ttc gcc tgc ctc taaaactgtc 238  
 Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu  
 65 70 75  
 atgatgtctt ctctctccct c 259

<110> 198  
 <111> 76  
 <112> P87  
 <113> *Conus gloriamaris*

<400> 198

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
 20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu  
 35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn  
 50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu  
 65 70 75

<110> 199  
 <111> 24  
 <112> P87  
 <113> *Conus gloriamaris*

<120>

<121> SITE

<122> (1) .. (24)

<123> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or  
 bromo-Trp

<400> 199

Cys Xaa Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser  
 1 5 10 15

Gly Xaa Cys Ile Phe Ala Cys Leu  
 20



<210> 200  
 <211> 288  
 <212> 1NA  
 <213> Conus dalli

<220>  
 <221> C1F  
 <222> 11... (228)

<230> 230  
 atg aag atg aag tgc att atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Ile Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttc gtc aag gct gtg cct cac tcc agc aat gag ttg gag aat 96  
 Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
 20 25 30

ctt tat atg aag gca cat cat gaa atg aac aac ccc gag gac tct gaa 144  
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu  
 35 40 45

tgg aac aag aag tgc tat gat ggt ggg aca ggt tgt gac tct gga aac 192  
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn  
 50 55 60

caa tcc tcc aat gcc tgg tgc att ttc gtc tgc ctc taaaaactgcc 238  
 Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Cys Leu  
 65 70 75

ggaggtat cctccacatc 258

<210> 211  
 <211> 291  
 <212> PRT  
 <213> Conus dalli

<220>

Met Lys Leu Thr Cys Ile Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn  
 20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu  
 35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn  
 50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Cys Leu  
 65 70 75

<210> 202  
 <211> 24  
 <212> PRT  
 <213> Conus dalli

<220>  
 <221> SITE  
 <222> (1)...(24)  
 <223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or bromo-Trp

<400> 202

Cys Xaa Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser  
 1 5 10 15

Gly Xaa Cys Ile Phe Val Cys Leu  
 20

<210> 203  
 <211> 203  
 <212> DNA  
 <213> Conus pennaceus

<220>  
 <221> GDS  
 <222> (1)...(228)

<400> 204  
 atg aaa atg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc aac aag cgg ttg gag aat 96  
 Trp Thr Val Val Thr Ala Val Pro His Ser Asn Lys Arg Leu Ala Asn  
 20 25 30

cct tat atg aag gca cgt cac gaa atg aaa aac ccc gaa gcc tct aat 144  
 Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn  
 35 40 45

gtg gac aag agg tgc ttt gag agt tgg gta gct tgt gag tct cca aaa 192  
 Val Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys  
 50 55 60

cga tgc tgc agt cac gtg tgc ctt ttc gtc tgc acc tgaaactgcc 238  
 Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr  
 65 70 75

ggagtgctct ctcctccct c 259

<210> 204  
 <211> 76  
 <212> PFI  
 <213> Conus pennaceus

<400> 204

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Val Val Thr Ala Val Pro His Ser Asn Lys Arg Leu Ala Asn  
 20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn  
35 40 45

Val Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys  
50 55 60

Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr  
65 70 75

0210 - 205

0211 - 24

0212 - PRT

0213 - *Corvus pennaceus*

0210 -

0211 - SITE

0212 - (1) .. (14)

0213 - Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at r  
esidue 5 may be Trp or bromo-Trp; Xaa at residue 11 may be Pro o  
r hydroxy-Pro

0100 - 105

Cys Ile Xaa Ser Xaa Val Ala Cys Xaa Ser Xaa Lys Arg Cys Cys Ser  
1 5 10 15

His Val Cys Leu Phe Val Cys Thr  
21

0110 - 106

0111 - 103

0112 - DHA

0113 - *Corvus distans*

0110 -

0111 - CDS

0112 - (1) .. (128)

0100 - 106

atg aag atg aag tgt atg ttg atc atc gct gtg atg ttc atg aag gcc 48  
Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

ttt aag atc ttt aca aat gcg agt tac gcc aga agt aag cag aag cat 96  
Cys Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His  
20 25 30

act att atg aag tgg act gac aaa aac tcc aag ttg acc cag cgt tgc 144  
Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys  
35 40 45

aat gaa gct aaa gaa cat tgc aat aac aat cct gac tgc tgc agt gag 192  
Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu  
50 55 60

tgt tcc aat aag ttt gtc ggc aga tgc ttg tca gac tgatctgatg 233  
Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp  
65 70 75

tattttcttc ccata

207  
 70  
 PPT  
 Conus distans

207

Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His  
 20 25 30

Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys  
 35 40 45

Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu  
 50 55 60

Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp  
 65 70 75

208  
 29  
 PPT  
 Conus distans

20  
 SITE  
 (1) .. (29)  
 Xaa at residues 3, 6 and 17 may be Glu or gamma-carboxy-Glu; Xaa  
 at residue 12 may be Pro or hydroxy-Pro

208

Cys Asn Xaa Ala Gln Xaa His Cys Thr Gln Asn Xaa Asp Cys Cys Ser  
 1 5 10 15

Xaa Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp  
 20 25

209  
 319  
 DNA  
 Conus ammiralis

22  
 CDS  
 (1) .. (226)

209  
 atg aaa ctg acg tgc ctg atg atc gtt gct ctg ctg ttc ttg acc gcc  
 Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg asa ttc gtc acg gct gtg cct gac tcc agc aat gcg ttg gag aat 96  
 Trp Thr Phe Val Thr Ala Val Pro Asp Ser Ser Asn Ala Leu Glu Asn  
 20 25 30  
 att tat ctg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa 144  
 Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu  
 35 40 45  
 ttg aac aag aag tgc tat gat ggt ggg aca agt tgt aac act gga aac 192  
 Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn  
 50 55 60  
 caa tgc tgc agt ggc tgg tgc att ttc ctc tgc ctc taaaactgcc 238  
 Gln Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu  
 65 70 75  
 gtgat tctt ctattccct c 259

<210> 210  
 <211> 76  
 <212> FFT  
 <213> Conus ammiralis

<400> 210

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro Asp Ser Ser Asn Ala Leu Glu Asn  
 20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu  
 35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn  
 50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu  
 65 70 75

<210> 211  
 <211> 24  
 <212> FFT  
 <213> Conus ammiralis

<220>

<221> SITE

<222> 1 ... (24)

<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or  
 bromo-Trp

<400> 211

Cys Xaa Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser  
 1 5 10 15

Gly Xaa Cys Ile Phe Leu Cys Leu  
20

0210 - 213  
0211 - 236  
0212 - DNA  
0213 - Conus textile

0220 -  
0221 - CDS  
0222 - (25)..(255)

0400 - 212  
ggattacat aaaacatcac caag atg aaa ctg acg tgc atg atg atc gtt 51  
Met Lys Leu Thr Cys Met Met Ile Val  
1 5

gat atg atg ttc ttg acc gcc tgg aca ttc gtc acg gct ggg cct cac 99  
Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Ala Pro His  
10 15 20 25

tac agc att ggg ttg gag aat ctt tat ctg aag gca cat cat gaa atg 147  
Ser Ser Asn Ala Leu Glu Asn Leu Tyr Leu Lys Ala His His Glu Met  
30 35 40

tac aac pro gaa gcc tct gaa ttg aac aag agg tgc tat gat agt ggg 195  
Asn Asn Pro Glu Ala Ser Glu Leu Asn Lys Arg Cys Tyr Asp Ser Gly  
45 50 55

aca agt tgt aac act gga aac caa tgc tgc agt ggg tgg tgc att ttc 243  
Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp Cys Ile Phe  
60 65 70

gac tct ttc ctg taaaaactaac gtgatgtctt ctctccct c 286  
Val Ser Cys Leu  
75

0210 - 213  
0211 - 77  
0212 - P87  
0213 - Conus textile

0400 - 213

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Ala Pro His Ser Ser Asn Ala Leu Glu Asn  
20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Ala Ser Glu  
35 40 45

Leu Asn Lys Arg Cys Tyr Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn  
50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Ser Cys Leu  
65 70 75

<210> 214  
 <211> M5  
 <212> PPT  
 <213> Ccnus textile

<220>  
 <221> SITE  
 <222> (1)...(25)  
 <223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or bromo-Trp

<400> 214

Cys Xaa Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser  
 1 5 10 15

Gly Xaa Cys Ile Phe Val Ser Cys Leu  
 20 25

<210> 215  
 <211> 272  
 <212> DNA  
 <213> Ccnus gloriamaris

<220>  
 <221> CDS  
 <222> (1)...(252)

<400> 215  
 atg aaa ctg arg tgc atg atg atc gtt gct gtg ctg ttc ctg aca gcc 48  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat ctt 96  
 Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu  
 20 25 30  
 ttt tgg aaa tca cgt gac gaa atg gag gac ccc gaa gct tct aaa ttg 144  
 Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu  
 35 40 45  
 gag aaa agg gat tgc caa gca cta tgg gat tat tgt cca gta ccg ctc 192  
 Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu  
 50 55 60  
 ttg tca tgg ggt gat tgc tgc tat ggc tta atc tgt ggc cct ttc gtc 240  
 Leu Ser Ser Gly Asp Cys Cys Tyr Gly Leu Ile Cys Gly Pro Phe Val  
 65 70 75 80  
 tgc att gga tgg tgatgtcttc tactcccatc 272  
 Cys Ile Gly Trp

<210> 216  
 <211> 84  
 <212> PPT  
 <213> Ccnus gloriamaris

<400> 216

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu  
20 25 30

Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu  
35 40 45

Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu  
50 55 60

Leu Ser Ser Gly Asp Cys Cys Tyr Gly Leu Ile Cys Gly Pro Phe Val  
65 70 75 80

Cys Ile Gly Trp

1210 217  
1211 33  
1212 PFT  
1213 Conus gloriamaris

1220  
1221 SITE  
1222 (1)..(33)  
1223 Xaa at residues 6 and 33 may be Trp or bromo-Trp; Xaa at residues 9 and 21 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 27 may be Pro or hydroxy-Pro

1400 217

Asp Cys Gln Ala Leu Xaa Asp Xaa Cys Xaa Val Xaa Leu Leu Ser Ser  
1 5 10 15

Gly Asp Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Ile Gly  
20 25 30

Xaa

1210 218  
1211 275  
1212 DNA  
1213 Conus omaria

1220  
1221 CDS  
1222 (1)..(249)

1400 218  
atg aag ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttc gtc atg gct gat gac tcc aac aat gga ctg gca aat ctt 96



Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu  
 20 25 30  
 ttc tgc aaa tca cgt gac gaa atg gag gat acc gat cct tct aaa ttg 144  
 Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Thr Asp Pro Ser Lys Leu  
 35 40 45  
 gag aac aga aaa act tgc caa aga agg tgg gat ttt tgt cca gga tgc 192  
 Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser  
 50 55 60  
 ctc att gga gtg ata act tgc tgc ggt ggc tta atc tgt ttt ctg ttc 240  
 Leu Val Gly Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe  
 65 70 75 80  
 ttc tgc gtt tgatagtgat gatctttctcc tccct 275  
 Phe Cys Val

<210> 213  
 <211> 83  
 <212> PFT  
 <213> Conus omaria

<400> 213

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu  
 20 25 30

Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Thr Asp Pro Ser Lys Leu  
 35 40 45

Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser  
 50 55 60

Leu Val Gly Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe  
 65 70 75 80

Phe Lys Val

<210> 210  
 <211> 37  
 <212> PFT  
 <213> Conus omaria

<220>  
 <221> SITE  
 <222> (1) .. (32)  
 <223> Xaa at residue 7 may be Trp or bromo-Trp; Xaa at residue 10 may be  
 e Pro or hydroxy-Pro

<400> 220

Lys Thr Cys Gln Arg Arg Xaa Asp Phe Cys Xaa Gly Ser Leu Val Gly  
1 5 10 15

Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe Phe Cys Val  
20 25 30

02100 211  
02110 274  
02120 DNA  
02130 Conus dalli

02200  
02210 CDS  
02220 (1)..(246)

04000 211  
atg aag atg aag tgt gtg atg atc gtt gat gtg ctg ttc ctg aca gcc 48  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

atg aag ata gtc atg gct gat gac tcc aac aat gga ctg gag aat ctt 96  
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu  
20 25 30

atg atg aaa tta cgt gac gaa atg gag gac ccc gaa ggt tct aaa ttg 144  
Phe Ser Lys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu  
35 40 45

atg aag aag gat tgc caa gaa aaa tgg gat tat tgt cca gta cag ttc 192  
Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe  
50 55 60

atg aga atg agg tat tgc tgc gat ggc ttt atc tgt cca tct ttc ttc 240  
Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe  
65 70 75 80

tgc tct agatagtgat gtcttctctata ttccctctc 274  
Cys Ala

02100 202  
02110 FL  
02120 PFT  
02130 Conus dalli

04000 212

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu  
20 25 30

Phe Ser Lys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu  
35 40 45

Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe  
50 55 60

Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe  
 65 70 75 80

Cys Ala

110: 283  
 111: 31  
 112: FET  
 113: Genus dalli

120:  
 121: SITE  
 122: (1) (31)  
 123: Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue  
 6 may be Trp or bromo-Trp; Xaa at residues 8 and 13 may be Tyr, 1  
 21-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
 yr; Xaa at residues 10, 12 and 26 may be Pro or hydroxy-Pro

140: 283

Asp Cys Glu Xaa Lys Xaa Asp Xaa Cys Xaa Val Xaa Phe Leu Gly Ser  
 5 10 15

Arg Xaa Cys Cys Asp Gly Phe Ile Cys Xaa Ser Phe Phe Cys Ala  
 20 25 30

110: 284  
 111: 31  
 112: DNA  
 113: Genus dalli

120:  
 121: FDS  
 122: (1) (352)

140: 284  
 110 aaa atg acg tgc atg atg atc gtt gct gtg ttg ttc ctg aca gcc 48  
 111 Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 5 10 15

tgc acc ata gac atg gct gat gac tcc aac aat gga ctg gcg aat cat 96  
 112 Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His  
 20 25 30

ttt tgg aaa tca cgt gac gaa atg gag gac cct gaa gct tct aaa ttg 144  
 113 Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu  
 35 40 45

gag aaa agg gat tgc caa ggc gaa tgg gag ttt tgt ata gta cgg gtc 192  
 114 Glu Lys Arg Asp Cys Glu Gly Glu Trp Glu Phe Cys Ile Val Pro Val  
 50 55 60

ctc gga ttt gtg tat tgc tgc ccc tgg ctt atc tgt ggc cct ttc gtc 240  
 115 Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val  
 65 70 75 80

tgc gtt gat atc tgaatgtcttc tatcccttc 271  
 Cys Val Asp Ile

00100 225  
 00110 84  
 00120 PWT  
 00130 Conus dalli

04000 225

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His  
 20 25 30

Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu  
 35 40 45

Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val  
 50 55 60

Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val  
 65 70 75 80

Cys Val Asp Ile

00100 226  
 00110 84  
 00120 PWT  
 00130 Conus dalli

00100 SITE  
 00110 1)..(33)  
 00120 Xaa at residues 5 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidues 6 and 22 may be Trp or bromo-Trp; Xaa at residues 12, 21  
 and 27 may be Pro or hydroxy-Pro;

00100 SITE  
 00110 1)..(33)  
 00120 Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-T  
 yr, C-sulpho-Tyr or O-phospho-Tyr

04000 226

Asp Cys Gln Gly Xaa Xaa Xaa Phe Cys Ile Val Xaa Val Leu Gly Phe  
 5 10 15

Val Xaa Cys Cys Xaa Xaa Leu Ile Cys Gly Xaa Phe Val Cys Val Asp  
 20 25 30

Ile

<210> 277  
 <211> 275  
 <212> ENA  
 <213> Cinus pennaceus

<220>  
 <221> CDS  
 <222> (1)..(234)

<400> 277  
 atg aaa atg acg tgc ctg atg atc att gct gtc ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Leu Met Ile Ile Ala Val Leu Phe Leu Thr Ala  
 5 10 15  
 tag gaa ttc gtc atg gct gat gac ccc aga gat gaa ccg gag gca cgt 96  
 Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg  
 20 25 30  
 atg gaa atg aac ccc gca gcc tct aaa ttg aac gag aga ggc tgc ctt 144  
 Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu  
 35 40 45  
 aa att gat tat ttt tgc ggc ata ccc ttt gtg aac aac ggg cta tgc 192  
 Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys  
 50 55 60  
 tgc agt agc aat tgt ggt ttt gtc tgc aca ccc caa ggg aag 234  
 Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys  
 65 70 75  
 aaaaatgctgtgtgatgtcttt ctctttcccat c 265

<210> 278  
 <211> 75  
 <212> PFT  
 <213> Cinus pennaceus

<400> 278

Met Lys Leu Thr Cys Leu Met Ile Ile Ala Val Leu Phe Leu Thr Ala  
 5 10 15  
 Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg  
 20 25 30  
 Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu  
 35 40 45  
 Hu Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys  
 50 55 60  
 Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys  
 65 70 75

<210> 279  
 <211> 61  
 <212> PFT  
 <213> Cinus pennaceus

4220: SITE  
 4221: (1) .. (31)  
 4222: Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue  
 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydrox  
 y-Pro

4400: 239

Gly Cys Leu Xaa Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn  
 1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln  
 20 25 30

4210: 230

4211: 478

4212: DNA

4213: *Conus marmoreus*

4220:

4221: 310

4222: (1, 2) .. (229)

4400: 239

gttgacatc atcaccatcg atccatctgt ccaccatct gtccatccat ccattccattc 60

attcactgac aaactgcat aaatatttga gtctctcttt ctgtttttat ctgacagatt 120

g aac gag aga gac tgc ctt aat gtt gat tat ttt tgc ggc ata ccg ttt 169  
 Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe  
 1 5 10 15

gtg aac aac ggg cta tgc tgc agt ggc aat tgt gtt ttt gtc tgc aca 217  
 Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr  
 20 25 30

tta aac ggg aag taaaactgcc gtgatgtctt ctcttccct ctagtagtag 269  
 Pro Gln Gly Lys  
 35

tagggggcgg ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt 329

ctatgtctc acctaaattc aattcactgg ccgtccgttt tacaacgtcg tgactgggaa 339

aacctggcgg ttaccgaact taatgcctt gcagcacat 428

4210: 231

4211: 36

4212: FFT

4213: *Conus marmoreus*

4400: 231

Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe  
 1 5 10 15

Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr  
 20 25 30

Pro Gln Gly Lys  
25

<210> 231  
<211> 30  
<212> PRT  
<213> *Conus marmoreus*

<210>  
<211> SITE  
<212> ... (30)  
<213> Xaa at residue 6 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 11 and 29 may be Pro or hydroxy-Pro

<400> 231

Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn Gly  
1 5 10 15  
Leu Lys Lys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln  
20 25 30

<210> 231  
<211> 30  
<212> DNA  
<213> *Conus marmoreus*

<220>  
<221> 203  
<222> (105)..(224)

<400> 231  
ccgacatgac caticatcgat ccatctgtcc atccatccat tcatttcattc gctgccaaac 60  
cgcataaatt attgagatct ctctttctgt ttttatctga caga ttg gac aag aga 116  
Leu Asp Lys Arg  
1  
gag tgc cag gaa gct gat tat tat tgc gtc tta ccg ttt gtg ggc aac 164  
Gln Lys Leu Glu Ala Asp Tyr Tyr Cys Val Leu Pro Phe Val Gly Asn  
5 10 15 20  
ggg atg tgc tgc agt ggc att tgt gtt ttt gtc tgc ata gcc caa cgc 212  
Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg  
25 30 35  
ttt aaa aac gtc tga 227  
Phe Lys Thr Val  
40

<210> 231  
<211> 40  
<212> PRT  
<213> *Conus marmoreus*

<400> 231

Leu Asp Lys Arg Glu Cys Leu Glu Ala Asp Tyr Tyr Cys Val Leu Pro

1                      5                      10                      15  
 Phe Val Gly Asn Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys  
                     20                      25                      30

Ile Ala Gln Arg Phe Lys Thr Val  
                     35                      40

<210> 235  
 <211> P6  
 <212> PET  
 <213> Conus marmoreus

<220>  
 <221> SITE  
 <222> (1)..(36)  
 <223> Xaa at residues 1 and 4 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidues 7 and 8 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr  
 , O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 12 may be Pro or  
 hydroxy-Pro

<400> 125

Xaa Lys Leu Xaa Ala Asp Xaa Xaa Cys Val Leu Xaa Phe Val Gly Asn  
 1                      5                      10                      15

Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg  
                     20                      25                      30

Phe Lys Thr Val  
                     35

<210> 236  
 <211> BL1  
 <212> DWA  
 <213> Conus marmoreus

<210>  
 <211> 233  
 <212> (1:1)..(241)

<400> 236  
 gtaagggtat ggaattcccg ggtcgacatc atcatcatcg atccatctgt ccattccatcc 60  
 atgattcatc tcatctcgctg ccaaaactgta ataaacattt gactctctct ttctgttttt 120  
 atctgacaga ttg aac gag aga gac tgc ctt gaa cct gat tat gtt tgc 169  
                     Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys  
                     1                      5                      10  
 ggc ata cgc ttt ggc ttc aac ggg cta tgc tgc agt gga att tgt gtt 217  
 cly il+ Pro Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val  
                     15                      20                      25  
 ttt at+ tgc ata ggc caa aag tat taaaaagcgc tgaatgtcttc tattcccatc 271  
 ile ile Cys ile Ala Gln Lys Tyr  
 31                      35  
 tagtagtagt aggcgggcgc tctagaggat ccaagcttac gtacgcgtgc atgcgacgta 331



atagctcttc tatagtgtca cctaaattca attcactggc cgtcgtttta caacgtcgtg 391  
 actgggaaaa ccttggcggtt acccaactta atcgcccttg agcaacatccc cctttcgcca 451  
 gctgcggt'aa tagcgcgaaga ggcccgccacc gatcgccctt ccccaacagtt ggcgcagcctg 511  
 aatgcgcgaat gggg 525

<210> 137  
 <211> 37  
 <212> FRT  
 <213> Conus marmoreus

<400> 137

Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys Gly Ile Pro  
 1 5 10 15

Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val Phe Ile Cys  
 20 25 30

Ile Ala Gln Lys Tyr  
 35

<210> 138  
 <211> 38  
 <212> FRT  
 <213> Conus marmoreus

<220>  
 <221> SITE  
 <222> 1)..(33)  
 <223> Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residues  
 5 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 33 may  
 be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-  
 -phospho-Tyr

<400> 138

Asp Tyr Leu Xaa Xaa Asp Xaa Val Cys Gly Ile Xaa Phe Val Phe Asn  
 1 5 10 15

Gly Leu Cys Cys Ser Gly Ile Cys Val Phe Ile Cys Ile Ala Gln Lys  
 20 25 30

Xaa

<210> 139  
 <211> 39  
 <212> DNA  
 <213> Conus marmoreus

<220>  
 <221> DS  
 <222> 1146)..(247)

<400> 239  
 ggtagcctg caggtaccg tccggaatto cggggtcgac atcatcatca tcatcgatcc 60

atctgtccat ccatttatctc attcatttcgc tgtcaaaactg taatacatat tagaatctct 120

cttctctgttt gttatctgaca gatttg gag aaa agg gcg tgc agc aaa aaa tgg 172  
 Glu Lys Arg Ala Cys Ser Lys Lys Trp  
 1 5

gaa tat tgt ata gta ccg atc ctt gga ttc gta tat tgc tgc cct ggc 220  
 Glu Tyr Cys Ile Val Pro Ile Leu Gly Phe Val Tyr Cys Cys Pro Gly  
 10 15 20 25

tta atc tgt ggt cct ttc gtc tgc gtt tgatagtga gtcttctcct 267  
 Leu Ile Cys Gly Pro Phe Val Cys Val  
 30

ccattctagt agtagtaggc ggcgcctcta gaggatccaa gcttaacgtac gcgtgcattgc 327

gaagtcattag ctctctctata gtgtcacccta aattcaattc actggccgctc gttttacaac 387

gttgtgaattg ggaaaacctt ggcgttaccc aacttaatcg ccttgcagca cctccctctt 447

tcgcagcttg gcgttaataag cgaagaggcc cgcaccgata gcccttccca acagttgcgc 507

agcctgaattg gcgaaatggg acgcgccttg 537

<210> 140

<211> 34

<212> PBT

<213> Conus marmoreus

<400> 140

Glu Lys Arg Ala Cys Ser Lys Lys Trp Glu Tyr Cys Ile Val Pro Ile  
 1 5 10 15

Leu Gly Phe Val Tyr Cys Cys Pro Gly Leu Ile Cys Gly Pro Phe Val  
 20 25 30

Cys Val

<210> 141

<211> 34

<212> PBT

<213> Conus marmoreus

<220>

<221> SITE

<222> 1) .. (31)

<223> Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residue 7 may be  
 Glu or gamma-carboxy-Glu; Xaa at residues 8 and 18 may be Tyr, 1  
 25-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
 yr; Xaa at residues 12, 21 and 27 may be Pro or hydroxy-Pro

<400> 241

Ala Cys Ser Lys Lys Xaa Xaa Xaa Cys Ile Val Xaa Ile Leu Gly Phe  
 1 5 10 15

Val Xaa Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Val  
 20 25 30

<210> 241  
 <211> 582  
 <212> DNA  
 <213> Conus omaria

<220>  
 <221> CDS  
 <222> (149)..(271)

<400> 242  
 aaagccggga cgcctgcagg tacgggtccg gaattcccg gtcgacatca tcatcatcat 60  
 cgtatcatct gtccatccat ccattcattc attcaactgcc aaactgtcat aaatatttga 120  
 gtctctcttt ctgtttttat ctgacaga ttg aac gag aga gac tgc ctt aat 172  
 Leu Asn Glu Arg Asp Cys Leu Asn  
 1 5  
 ggt gat tat ttt tgt ggc ata ccg ttt gtg aac aac ggg cta tgc tgc 220  
 Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys Cys  
 10 15 20  
 agt ggc tat tgt gtt ttt tgt ctg cac acc cca agg gaa gta aaa ctg 268  
 Ser Gly Asn Cys Val Phe Cys Leu His Thr Pro Arg Glu Val Lys Leu  
 25 30 35 40  
 ccg tgatgtcttc tcttcccttc tagtagtagt aggcggccgc tetagaggat 321  
 Pro  
 ccaagcttac gtaacggtgc atgagacgtc atagctcttc tatagtgtca cctaaattca 381  
 attractgac cgtcgtttta caacgtcgtg actgggaaaa ccttggcgtt acccaactta 441  
 atgccttttc agcacatccc cctttcgcca gctggcgtaa tagcgaagag gcccgcaccg 501  
 atgcctcttc ccaacagtgt cgcagcctga atggcgaatg ggacgcgcgc t 552

<210> 143  
 <211> 41  
 <212> PRT  
 <213> Conus omaria

<400> 143

Leu Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro  
 1 5 10 15

Phe Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu  
 20 25 30

His Thr Pro Arg Glu Val Lys Leu Pro  
 35 40

<210> 144  
 <211> 37  
 <212> PRT

01130 Conus emaria

01100

01110 SITE

01120 (1)...(37)

01130 Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12, 31 and 37 may be Pro or hydroxy-Pro; Xaa at residue 33 may be Glu or gamma-carboxy-Glu

04000 044

Asp Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn  
1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu His Thr Xaa Arg  
20 25 30

Met Val Lys Leu Xaa  
35

01100 045

01110 SITE

01120 RNA

01130 Conus obscurus

01200

01210 SITE

01220 (186)...(181)

04000 045

atattcattat gtgcattccat ccattccattc attcattgtcc aaactgtaac aaatattcaa 60

actattcatt ctgtttgtgt ctgac aga tgc aaa cgg tgc att gtt tac ggt 112  
Arg Ser Lys Arg Cys Leu Val Tyr Gly  
1 5

aaa gct tgt gac tgg ctg acc att ggg ggt atg gag tgc tgc agt aaa 160  
Thr Pro Cys Asp Trp Leu Thr Ile Ala Gly Met Glu Cys Cys Ser Lys  
1 15 20 25

agg tgc ttt atg atg tgc tgg taaaactgcc gtgatgtatt ctactccct c 212  
Lys Cys Phe Met Met Cys Trp  
30

01110 046

01120 SITE

01130 RNA

01140 Conus obscurus

04000 046

Arg Ser Lys Arg Cys Leu Val Tyr Gly Thr Pro Cys Asp Trp Leu Thr  
5 10 15

Ile Ala Gly Met Glu Cys Cys Ser Lys Lys Cys Phe Met Met Cys Trp  
20 25 30

01100 047

01110 SITE

<212> PBT  
<213> *Conus obscurus*

<220>  
<221> SITE  
<222> (1)...(28)  
<223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or hydroxy-Pro; Xaa at residues 10 and 28 may be Trp or bromo-Trp; Xaa at residue 17 may be Glu or gamma-carboxy-Glu

<400> 247

Cys Leu Val Xaa Gly Thr Xaa Cys Asp Xaa Leu Thr Ile Ala Gly Met  
1 5 10 15  
Xaa Cys Cys Ser Lys Lys Cys Phe Met Met Cys Xaa  
20 25

<212> 248  
<213> 139  
<214> DCA  
<215> *Conus radiatus*

<220>  
<221> SITE  
<222> (1)...(109)

<400> 248 49  
a atg aat cag aga gac tgc cat gaa gtt ggt gaa ttt tgt ggc tta ccg  
1 5 10 15  
Leu Asn Gln Arg Asp Cys His Glu Val Gly Glu Phe Cys Gly Leu Pro  
20 25 30  
tta ata aag aac ggg cta tgc tgc agt cag att tgt tta ggt gtc tgc  
1 5 10 15 20 25 30  
Leu Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys  
35 40 45 50 55 60  
aaa aag ttt taaaactgcc gtgatgtctt ctactcccat  
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 139  
Ala Lys Val Phe

<212> 249  
<213> 140  
<214> PBT  
<215> *Conus radiatus*

<400> 249

Leu Asn Gln Arg Asp Cys His Glu Val Gly Glu Phe Cys Gly Leu Pro  
1 5 10 15  
Leu Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys  
20 25 30

Ala Lys Val Phe  
35

<L10> 160  
<L11> 162

<212> FET  
<213> Conus radiatus

<220>  
<221> SITE  
<222> (1)...(32)  
<223> Xaa at residues 4 and 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Pro or hydroxy-Pro

<400> 250

Asp Cys His Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn  
1 5 10 15  
Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys Ala Lys Val Phe  
20 25 30

<212> 251  
<213> 133  
<214> RNA  
<215> Conus radiatus

<221>  
<222> FDS  
<223> 1... (100)

<400> 251  
t tta gtt aag aaa gag tgc act gcc aat ggt gaa ttt tgt ggc ata tcg 49  
Leu Asp Lys Lys Glu Cys Thr Ala Asn Gly Glu Phe Cys Gly Ile Ser  
1 5 10 15  
ggt att gga agc tac cta tgc tgc agt ggc cgg tgt gta ttc gtc tgc 97  
Val Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys  
20 25 30  
atc tagtgaact gccgtgatgt ettctactcc cct 133  
ile

<212> 252  
<213> 133  
<214> FET  
<215> Conus radiatus

<400> 252

Leu Asp Lys Lys Glu Cys Thr Ala Asn Gly Glu Phe Cys Gly Ile Ser  
1 5 10 15  
Val Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys  
20 25 30

Ile

<212> 253  
<213> 133  
<214> FET  
<215> Conus radiatus

<220>  
 <221> SITE  
 <222> 1)...(29)  
 <223> Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r  
 esidue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su  
 lpho-Tyr or O-phospho-Tyr

<400> 153

Xaa Cys Thr Ala Asn Gly Xaa Phe Cys Gly Ile Ser Val Phe Gly Ser  
 1 5 10 15

Xaa Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys Ile  
 20 25

<210> 254  
 <211> 133  
 <212> DNA  
 <213> Conus radiatus

<220>  
 <221> SITE  
 <222> 1)...(100)

<400> 174  
 1...: gtc aag aaa gag tgc act acc aat ggt gaa ttt tgt ggc ata tgc 49  
 Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser  
 1 5 10 15

gtc ttt gca agc ttc cta tgc tgc agt ggc ctg tgt gta ttc gtc tgc 97  
 Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys  
 20 25 30

atc tagatgaact gccgtgatgt cttctctttcc cct 133  
 Ile

<210> 255  
 <211> 13  
 <212> PBT  
 <213> Conus radiatus

<400> 255

Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser  
 1 5 10 15

Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys  
 20 25 30

Ile

<210> 256  
 <211> 13  
 <212> PBT  
 <213> Conus radiatus

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(29)

&lt;223&gt; Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu.

&lt;400&gt; 256

Xaa	Cys	Thr	Thr	Asn	Gly	Xaa	Phe	Cys	Gly	Ile	Ser	Val	Phe	Ala	Ser
1				5					10					15	

Phe	Leu	Cys	Cys	Ser	Gly	Leu	Cys	Val	Phe	Val	Cys	Ile
		20					25					

&lt;110&gt; 257

&lt;111&gt; 173

&lt;112&gt; DNA

&lt;113&gt; Conus radiatus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(100)

&lt;400&gt; 257

1	att	gac	aag	aga	aaa	tgc	ttt	ccc	aaa	aat	cat	ttt	tgt	ggc	ttt	gtg	49
	Leu	Asp	Lys	Arg	Lys	Cys	Phe	Pro	Lys	Asn	His	Phe	Cys	Gly	Phe	Val	
1				5					10					15			

1	gtg	atg	ctg	aac	tac	cta	tgc	tgc	agt	ggc	cgg	tgt	ata	ttc	gtc	tgc	97
	Val	Met	Leu	Asn	Tyr	Leu	Cys	Cys	Ser	Gly	Arg	Cys	Ile	Phe	Val	Cys	
			20					25					30				

1	gac	tac	gtt	gaa	act	gac	gtg	gat	gtg	att	tac	act	ccc	cat
	Val													
														133

&lt;110&gt; 253

&lt;111&gt; 33

&lt;112&gt; EST

&lt;113&gt; Conus radiatus

&lt;400&gt; 253

Leu	Asp	Lys	Arg	Lys	Cys	Phe	Pro	Lys	Asn	His	Phe	Cys	Gly	Phe	Val
1				5					10					15	

Val	Met	Leu	Asn	Tyr	Leu	Cys	Cys	Ser	Gly	Arg	Cys	Ile	Phe	Val	Cys
			20				25					30			

Val

&lt;110&gt; 259

&lt;111&gt; 29

&lt;112&gt; PFT

&lt;113&gt; Conus radiatus

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(29)



<223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 109

Lys Cys Phe Xaa Lys Asn His Phe Cys Gly Phe Val Val Met Leu Asn  
1 5 10 15

Xaa Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys Val  
20 25

<210> 109

<211> 130

<212> DNA

<213> Conus regius

<220>

<221> CDS

<222> (1)..(99)

<400> 160

atg tac aag aga agc tgc ctt cct cta gac tgg ttt tgt ggc ttc aat 48  
Leu Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Asn  
1 5 10 15

aaa att aga agg ttt ctg tgc tgt agt ggc tac tgc ctt gtc gtc tgc 96  
Ile Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys  
20 25 30

atg aaaaatggc gtgatgtatt ctctccccc c 130  
Met

<210> 261

<211> 37

<212> PRT

<213> Conus regius

<400> 261

Leu Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Asn  
1 5 10 15

Ile Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys  
20 25 30

Met

<210> 262

<211> 29

<212> PRT

<213> Conus regius

<220>

<221> SITE

<222> (1)..(29)

<223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may

be Trp or bromo-Trp; Xaa at residue 23 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, C-sulpho-Tyr or O-phospho-Tyr

<400> 262

Ser Cys Leu Xaa Leu Asp Xaa Phe Cys Gly Phe Asn Ile Ile Gly Ala  
1 5 10 15

Phe Leu Cys Cys Ser Gly Xaa Cys Leu Val Val Cys Met  
20 25

<210> 263

<211> 314

<212> DNA

<213> *Genus delessertii*

<220>

<221> 303

<222> (1) .. (285)

<400> 263

atg aaa ctg aag tgt ctg ctg atc gtt gct gtg ctg gtc ttg gca gcc 48  
Met Lys Leu Thr Cys Leu Leu Ile Val Ala Val Leu Val Leu Ala Ala  
1 5 10 15

tgt cag ttc atc gta gct ggc gac tcc agt gat ggc cag gag aat cct 96  
Cys Gln Phe Ile Val Ala Gly Asp Ser Ser Asp Gly Gln Glu Asn Pro  
20 25 30

gct ctg agg tca cct agc gat tcc tct ggg aaa atg tca tca atg aag 144  
Ala Leu Arg Ser Pro Ser Asp Ser Ser Gly Lys Met Ser Ser Met Lys  
35 40 45

agg ttc cag aaa cgg ctg atg gtg ggg caa tct gca tcc aaa aga cca 192  
Arg Phe Gln Thr Arg Leu Met Val Gly Gln Ser Ala Ser Lys Arg Pro  
50 55 60

agg aag agg gac tgc atc ccc ggc ggc gaa aat tgt gat gta ttc cga 240  
Ser Lys Arg Asp Cys Ile Pro Gly Gly Gln Asn Cys Asp Val Phe Arg  
65 70 75 80

cca tac agg tgc tgc agt gga tat tgc ata cta ctc ctt tgc gca 285  
Pro Tyr Arg Cys Cys Ser Gly Tyr Cys Ile Leu Leu Leu Cys Ala  
85 90 95

tgataaagct gcttgatgt cttctctccc cctc 319

<210> 364

<211> 36

<212> F&T

<213> *Genus delessertii*

<400> 264

Met Lys Leu Thr Cys Leu Leu Ile Val Ala Val Leu Val Leu Ala Ala  
1 5 10 15

Cys Gln Phe Ile Val Ala Gly Asp Ser Ser Asp Gly Gln Glu Asn Pro  
20 25 30

Ala Leu Arg Ser Pro Ser Asp Ser Ser Gly Lys Met Ser Ser Met Lys  
25 40 45

Arg Ile Gln Thr Arg Leu Met Val Gly Gln Ser Ala Ser Lys Arg Pro  
50 55 60

Ser Lys Arg Asp Cys Ile Pro Gly Gly Glu Asn Cys Asp Val Phe Arg  
65 70 75 80

Pro Tyr Arg Cys Cys Ser Gly Tyr Cys Ile Leu Leu Leu Cys Ala  
85 90 95

<10> 265  
<11> 28  
<12> PRT  
<13> Genus delessertii

<20>  
<21> SITE  
<22> (1)..(28)  
<23> Xaa at residues 4 and 14 may be Pro or hydroxy-Pro; Xaa at residue  
4 7 may be Glu or gamma-carboxy-Glu; Xaa at residues 15 and 21 ma  
y be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
O-phospho-Tyr

<40> 266  
Asp Cys Ile Xaa Gly Gly Xaa Asn Cys Asp Val Phe Arg Xaa Xaa Arg  
5 10 15  
Cys Cys Ser Gly Xaa Cys Ile Leu Leu Leu Cys Ala  
20 25

<10> 1006  
<11> 1009  
<12> DNA  
<13> Genus striatus

<20>  
<21> CDS  
<22> (147)..(233)

<20>  
<21> misc\_feature  
<22> (1)..1009  
<23> n may be any nucleotide

<40> 266  
gctggttcgc cgcaggtac cgtccggaa ttcccggtc gacatcatca tcacgatcc 60  
atctgtccat ccatctattc attcattcat tcgctgccaa actgtattaa atattcaagt 120  
ctctttttct gtttgtgtct aacaga ttg aga tgg tgc att cct agt ggt gaa 173  
Leu Arg Trp Cys Ile Pro Ser Gly Glu  
1 5  
att tgt ttc cgc tgc gat cac ata gga tgc tgc agt ggc aag tgc gca 221  
Leu Cys Phe Arg Ser Asp His Ile Gly Cys Cys Ser Gly Lys Cys Ala

0010: 207  
 0011: 24  
 0012: FFT  
 0013: Genus striatus

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<221   misc_feature
<221   1)..(1009)
<224   n may be any nucleotide

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&lt;400&gt; 2:7

Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys Phe Arg Ser Asp His  
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
20 25

```
<210> 158
<211> 19
<212> 1RT
<213> Conus triatus
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<216>
<217> SITE
<218> 1)...(19)
<223> Xaa at residue3 may be Trp or bromo-Trp; Xaa at residue 6 may be
Pro or hydroxy-Pro; Xaa at residue 9 may be Glu or gamma-carboxy
-Glu

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&lt;400&gt; 268

Leu Arg Xaa Cys Ile Xaa Ser Gly Xaa Leu Cys Phe Arg Ser Asp His  
 1 5 10 15  
 Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

&lt;210&gt; 269

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Conus striatus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(87)

&lt;400&gt; 269

aaa aga tgg tgc att cct agt ggt gat ctt tgt ttc cgc tgc gat cac 48  
 Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His  
 1 5 10 15  
 aaa aga tgc tgc agt ggc aag tgc gca ttc gtc tgc ttg taa 90  
 Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

&lt;210&gt; 170

&lt;211&gt; 29

&lt;212&gt; 1FT

&lt;213&gt; Conus striatus

&lt;400&gt; 170

Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His  
 1 5 10 15  
 Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

&lt;210&gt; 171

&lt;211&gt; 27

&lt;212&gt; 1FT

&lt;213&gt; Conus striatus

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)... 27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be  
 Pro or hydroxy-Pro

&lt;400&gt; 271

Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Arg Ser Asp His Ile Gly  
 1 5 10 15  
 Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

<210> 272  
 <211> 89  
 <212> DNA  
 <213> *Conus striatus*

<220>  
 <221> CDS  
 <222> (1)..(37)

<400> 272  
 ttg aga tgg tgc att cct agt ggt gat ctt tgt ttc cgc tcg gat cac 48  
 Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His  
 1 5 10 15  
 ata aaa tgc tgc agt ggc aag tgc gca ttc gtc tgc ttg taa 90  
 Ile Gln Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

<210> 273  
 <211> 89  
 <212> PPT  
 <213> *Conus striatus*

<400> 273  
 Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His  
 1 5 10 15

Ile Gln Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

<210> 274  
 <211> 89  
 <212> PPT  
 <213> *Conus striatus*

<220>  
 <221> S1IE  
 <222> (1)..(27)  
 <223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be  
 Pro or hydroxy-Pro

<400> 274

Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Arg Ser Asp His Ile Gln  
 1 5 10 15

Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu  
 20 25

<210> 275  
 <211> 86  
 <212> DNA  
 <213> *Conus obscurus*

<220>  
 <221> IDS  
 <222> (77)..(175)

<400> 275

ccattccatct gtccatccat ccattcagtc attcgctgcc aaactgtaac aaatattcaa 60  
 gtcttgcttt ctgttt gtg tct gac aga ttg aga tgg tgc gtt cct agc ggt 112  
                   Val Ser Asp Arg Leu Arg Trp Cys Val Pro Ser Gly  
                   1                  5                  10  
 gaa gtt tgt cgc cgc tat gaa ttc gtg gga tgc tgc agt ggc aag tgc 160  
 Glu Val Cys Arg Arg Tyr Glu Phe Val Gly Cys Cys Ser Gly Lys Cys  
                   15                  20                  25  
 ttc ttc gtc tgc tog taaaaactgtt gtgatgtctt ctctccct c 206  
 Phe Phe Val Cys Ser  
                   30

<110> 276  
 <111> ?  
 <112> PRT  
 <113> Genus obscurus

<400> 276

Val Ser Asp Arg Leu Arg Trp Cys Val Pro Ser Gly Glu Val Cys Arg  
 1                  5                  10                  15  
 Arg Tyr Glu Phe Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys  
                   20                  25                  30

Ser

<110> 277  
 <111> ?  
 <112> PRT  
 <113> Genus obscurus

<111>  
 <112> SITE  
 <113> (1) .. (2)  
 <120> Xaa at residue 3 may be Trp or bromo-Trp; Xaa at residue 6 may be  
           Pro or hydroxy-Pro; Xaa at residues 9 and 15 may be Glu or gamma  
           -carboxy-Glu; Xaa at residue 14 may be Tyr, 125-I-Tyr, mono-iodo-  
           Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 277

Leu Arg Xaa Cys Val Xaa Ser Gly Xaa Val Cys Arg Arg Xaa Xaa Phe  
 1                  5                  10                  15  
 Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys Ser  
                   20                  25

<110> 278  
 <111> 259  
 <112> DNA  
 <113> Conus radiatus

<220>  
 <221> CDS  
 <222> (22) .. (117)

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00100- 179
00110- 75
00120- PPT
00130- Genus radiatus

00200- 175

Arg Ver Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg
      5              10              15

Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
      20              25              30

00300- 180
00310- 18
00320- PPT
00330- Genus radiatus

00400-
00410- SITE
00420- 1) .. (18)
00430- Asa at residue 3 may be Pro or hydroxy-Pro.

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<210>      130
Cys Leu Lys Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1          5          10          15
Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
          20          25
<211>      131
<212>      478
<213>      DNA
<214>      Bonus geographus
<220>
<221>      DIS
<222>      "3'..(318)
<400>      131
ggaatcttgcacgggtgaatttcgcttcatat ttttctaactg tcgtttttgg catcatccaa
60

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aacatcacca ag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 111  
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe  
1 5 10

ttg acc gcc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta 159  
Leu Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val  
15 20 25

ttg gag aat ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa 207  
Leu Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu  
30 35 40 45

gcc tct aaa ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat 255  
Ala Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp  
50 55 60

ttt tgt gcc ttt ttt aaa att ggg cgg cct tgc tgc agt ggc tgg tgc 303  
Phe Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys  
65 70 75

tto cto tgg tgc gcc taaaactgcc gtgatgtctt ctattccct ctgtgtacc 358  
Phe Leu Trp Cys Ala  
80

tggcttgatc ttgattggc gctgcccctt cagtggttat gaacccccct gagccgactc 418  
tctgggggccc tcgggggttc aacatccaaa taaagcgaca acacaatcac aagtaaaaaa 478

<210> 282

<211> 31

<212> PFT

<213> *Onus geographus*

<400> 282

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn  
20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys  
35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly  
50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp  
65 70 75 80

Cys Ala

<210> 283

<211> 31

<212> PFT

<213> Conus geographus

<220>

<221> SITE

<222> 10..(30)

<223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 24 and 28 may be Trp or bromo-Trp

<400> 183

Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile  
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala  
20 25 30

<213> 184

<211> 18

<212> PWA

<213> Conus textile

<220>

<221> CHG

<222> 1..(164)

<223>

<224> misc\_feature

<225> 1..(318)

<226> n may be any nucleotide

<400> 284

gc tgc agt tog act cta gag ggc ttg gag aat ctt tat ctg aag gca 47  
Cys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala  
1 5 10 15

cat cat gaa atg aac aac ccc gaa gac tct gaa ttg aac aag agg tgc 95  
His His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys  
20 25 30

tat cat agt ggg aca agt tgt aac act gga aac gaa tgc tgc agt ggc 143  
Tyr Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly  
35 40 45

tgc tgc att ttc gtc tgc ctc taaaaactgac gtgatgtatt ctactccct 194  
Trp Cys Ile Phe Val Cys Leu  
50

ctactctaac tacttggttt gatctttgat tggcgogtgc ccttcaactgg ttatgaaccc 254

ctctctatccc actctctggtt ggcctggggg atccaaacatc aaaatanagc gacagcaciaa 314

tcaac 318

<213> 285

<211> 54

<212> PWT

<213> Conus textile

<220>

<221> misc\_feature

<222> (11..(318)

<223> n may be any nucleotide

<410> 285

Cys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala His  
1 5 10 15

His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys Tyr  
20 25 30

Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp  
35 40 45

Cys Ile Phe Val Cys Leu  
50

<11> 236

<11> 24

<12> PET

<13> Canis textile

<20>

<21> SITE

<22> (1)..(24)

<23> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, 3-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or bromo-Trp

<410> 286

Cys Xaa Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser  
1 5 10 15

Gly Xaa Cys Ile Phe Val Cys Leu  
20

<11> 247

<11> 493

<12> DCA

<13> Canis quercinus

<21>

<21> CDS

<22> (17)..(333)

<410> 287

gatttggtat' tctccctgtgt cttocttggc atcaccacaaa acatcaccas g atg aaa  
Met Lys  
1

atc acg tgc atg atg atc gtt gat ctg ctg ttc tgc aac gtt tgg aca  
Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala Trp Thr  
5 10 15

ttc gtc arg gct gtt gac tcc aaa aat gaa ctg gag aac aga gga gga  
Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg Gly Gly  
20 25 30

57

105

153

tgg ggg cag gca gga gga tgg ggg aaa ctt ttt ccg atg gca cgc gac 201  
 Trp Gly Gln Ala Gly Gly Trp Gly Lys Leu Phe Pro Met Ala Arg Asp  
 25 40 45 50

gaa atg aaa aac agc gaa gtc tct aaa ttg gac aat aag aga aag tgc 249  
 Glu Met Lys Asn Ser Glu Val Ser Lys Leu Asp Asn Lys Arg Lys Cys  
 55 60 65

gct aca gcc ggt gaa gct tgc gta ata cct atc att gga aac gta ttt 297  
 Ala Ala Ala Gly Glu Ala Cys Val Ile Pro Ile Ile Gly Asn Val Phe  
 70 75 80

tgc tgc aaa ggc tac tgt ctt ttc gtc tgc att agt taaactgctg 343  
 Cys Cys Lys Gly Tyr Cys Leu Phe Val Cys Ile Ser  
 85 90

tgatgacttc tactcaactc tgtgctactc ggcttgatct ttgattggcg tgtgcocttc 403

actgtttatg agcttgtctg atctactct ctggagacct ctgtggctca acatccaaat 463

aaagtgcat ccaaatg 480

<110> 283

<111> 94

<112> PPT

<113> Conus quercinus

<400> 283

Met Lys Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg  
 20 25 30

Gly Gly Trp Gly Gln Ala Gly Gly Trp Gly Lys Leu Phe Pro Met Ala  
 35 40 45

Arg Asp Glu Met Lys Asn Ser Glu Val Ser Lys Leu Asp Asn Lys Arg  
 50 55 60

Lys Cys Ala Ala Ala Gly Glu Ala Cys Val Ile Pro Ile Ile Gly Asn  
 65 70 75 80

Val Phe Cys Cys Lys Gly Tyr Cys Leu Phe Val Cys Ile Ser  
 85 90

<210> 283

<211> 29

<212> PPT

<213> Conus quercinus

<220>

<221> SITE

<222> (1)..(29)

<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue  
 11 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Tyr, 125-1

-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 339

Cys Ala Ala Ala Gly Kaa Ala Cys Val Ile Xaa Ile Ile Gly Asn Val  
1 5 10 15

Phe Cys Cys Lys Gly Kaa Cys Leu Phe Val Cys Ile Ser  
20 25

<210> 339

<211> 310

<212> DNA

<213> *Canis leopardus*

<220>

<221> CDS

<222> 111..(246)

<400> 106

atg aaa atg aag tgc gtg gtg atc gtt gct gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

acg ata ttc atc aag gct gat gac tcc aca aat gga ctg gag aat cgt 96  
Trp Ile Phe Ile Thr Ala Asp Asp Ser Thr Asn Gly Leu Glu Asn Arg  
20 25 30

ttt agg aag gca cgt gac aac atg aag aac gcc aaa gcc tct aca tta 144  
Phe Arg Lys Ala Arg Asp Asn Met Lys Asn Ala Lys Ala Ser Thr Leu  
35 40 45

ccc gag aag aaa gag tgt gtt gaa ctt gct gag att tgt gcc aca gcc 192  
Ala Glu Lys Lys Ala Cys Val Glu Leu Gly Glu Ile Cys Ala Thr Gly  
50 55 60

ttc ttc cta gac gag gaa tgc tgc act ggt tca tgc cat gtc ttc tgc 240  
Phe Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys  
65 70 75 80

gla cta tagttaaaact gctgtgatgt cttctttctct cctccgtgct acctggcttg 296  
Val Leu

atctttgat ggtgcctgtc ctccagtggt tgtgaaaacc tctgatccta ctctctggac 356

gcctctgac cccaacatcc aaataaagcg acatcctaata gccaaaaaaaa aaaa 410

<210> 191

<211> 1

<212> PRT

<213> *Canis leopardus*

<400> 241

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Ile Phe Ile Thr Ala Asp P p Ser Thr Asn Gly Leu Glu Asn Arg  
20 25 30

Phe Arg Lys Ala Arg Asp Asn Met Lys Asn Ala Lys Ala Ser Thr Leu  
 35 40 45

Ala Glu Lys Lys Ala Cys Val Glu Leu Gly Glu Ile Cys Ala Thr Gly  
 50 55 60

Phe Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys  
 65 70 75 80

Val Leu

01100- 242

01110- 30

01120- PPT

01130- *Conus leopardis*

01100-

01110- SITE

01120- 1... (20)

01130- Xaa at residues 4, 7, 17 and 18 may be Glu or gamma-carboxy-Glu.

01100- 192

Ala Cys Val Xaa Leu Gly Xaa Ile Cys Ala Thr Gly Phe Phe Leu Asp  
 1 5 10 15

Xaa Xaa Cys Cys Thr Gly Ser Cys His Val Phe Cys Val Leu  
 20 25 30

01100- 243

01110- 346

01120- DNA

01130- *Conus narmoreus*

01100-

01110- 313

01120- 1... (231)

01100- 243

atg aaa atg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttt gac acg gct gat gac ccc aga aat gga ttg gag aat ctt 96  
 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
 20 25 30

ttt tgg agg gaa cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

aac aag agg tgc cct aac act ggt gaa tta tgt gat gtg gtt gaa caa 192  
 Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln  
 50 55 60

aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta taaaactacc 241

Asn Lys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu  
65 70 75

atgagtgctt ctactccctt ctgtgtgtgc ttgcttgatc ttgtattggc gctgtccctt 301  
cactgtttat gacccccctg atccgacctc tggggg 336

<210> 294  
<211> 77  
<212> PPT  
<213> *Conus marmoreus*  
<400> 294

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln  
50 55 60

Asn Lys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu  
65 70 75

<210> 146  
<211> 26  
<212> PPT  
<213> *Conus marmoreus*

<220>  
<221> SITE  
<222> 11..(26)  
<223> Xaa at residue 2 may be Pro or hydroxy-Pro; Xaa at residues 6 and 12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or -phospho-Tyr

<400> 146

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys  
1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu  
20 25

<210> 146  
<211> 412  
<212> JNA  
<213> *Conus quercinus*

<220>  
<221> DIS

&lt;222&gt; 17) .. (240)

&lt;400&gt; 296

ggatcc atg aaa ctg acg tgt atg gtg atc gtt gct gtg cta ttc ttg 48  
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu  
 1 5 10

acc gcc tgg gct gat gac tcc aga aat gga ttc gag aat cga aat gga 96  
 Thr Ala Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly  
 15 20 25 30

gaa cga aac gaa aac gaa atg aag aac ctg gaa gcc tct aaa ttg aac 144  
 Glu Arg Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn  
 35 40 45

agg aga gac ggc gat tgc gtt gat ggt ggt gaa ttt tgt gcc ttt ccg 192  
 Arg Arg Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro  
 50 55 60

aaa att gga ggg cca tgc tgt agt ggc tgg tgc ttt ttc gtc tgc tta 240  
 Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu  
 65 70 75

taaaactgac atgatgtctt ctacccctct ctgtgtatcc tgacttgatc ttgattggc 300

gtgtgcccctt cactggttat gaacccctct gatccgactc tctggaggcc tcgggggtcc 360

aacatccaaa taaagcgaca gcaaaaaaaaa aaaaaaaaaa aa 402

&lt;210&gt; 297

&lt;211&gt; 78

&lt;212&gt; PFT

&lt;213&gt; Cinus quercinus

&lt;400&gt; 297

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly Glu Arg  
 20 25 30

Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn Arg Arg  
 35 40 45

Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro Lys Ile  
 50 55 60

Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu  
 65 70 75

&lt;210&gt; 298

&lt;211&gt; 31

&lt;212&gt; PFT

&lt;213&gt; Cinus quercinus

&lt;220&gt;

&lt;221&gt; SITE



<222> (1)..(30)  
 <223> Xaa at residue 9 may be Glu or gamma-carboxy-Glu; Xaa at residues  
 14 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp  
 or bromo-Trp

<400> 293

Asp Gly Asp Cys Val Asp Gly Gly Xaa Phe Cys Gly Phe Xaa Lys Ile  
 1 5 10 15

Gly Gly Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu  
 20 25 30

<210> 299

<211> 374

<212> DNA

<213> Genus quercinus

<220>

<221> CDS

<222> (1)..(216)

<220>

<221> misc\_feature

<222> (1)..(274)

<223> n may be any nucleotide

<400> 299

ggatgc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg cta ttc ttg 48  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
 1 5 10

acc gcc ttg ggt gat gac tcc aga aat gga ttg gag aat cga aat gaa 96  
 Thr Ala Leu Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Arg Asn Glu  
 15 20 25 30

caa gaa cga aac gaa aac gaa atg agg gac cgc cgg gac tgc caa gat 144  
 Gln Glu Arg Asn Glu Asn Glu Met Arg Asp Arg Arg Asp Cys Gln Asp  
 35 40 45

agt ggt gta gtt tgt ggc ttt cgc aaa cct gaa cca cac tgc tgc agt 192  
 Ser Gly Val Val Cys Gly Phe Pro Lys Pro Glu Pro His Cys Cys Ser  
 50 55 60

gcc tgg tgc ctt ttc gtc tgc gcc taaaaatgcc gtgatgtcaa atsaagcgac 246  
 Gly Trp Cys Leu Phe Val Cys Ala  
 65 70

acacaatnna aaaaaaaaaa aaaaaaaaaa 274

<210> 300

<211> 71

<212> FRT

<213> Genus quercinus

<220>

<221> misc\_feature

<222> (1)..(274)

<223> n may be any nucleotide

<400> 300

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Leu Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Arg Asn Glu Gln Glu  
20 25 30

Arg Asn Glu Asn Glu Met Arg Asp Arg Arg Asp Cys Gln Asp Ser Gly  
35 40 45

Val Val Lys Gly Phe Pro Lys Pro Glu Pro His Cys Cys Ser Gly Trp  
50 55 60

Cys Leu Phe Val Cys Ala  
65 70

<110> P01  
<111> 14  
<112> EST  
<113> *Onchus quercinus*

<120>  
<121> SITE  
<122> 1) .. (28)  
<123> Xaa at residues 12, 14 and 16 may be Pro or hydroxy-Pro; Xaa at r  
esidue 15 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may b  
e Trp or bromo-Trp

<100> P01

Asp Cys Gln Asp Ser Gly Val Val Cys Gly Phe Xaa Lys Xaa Xaa Xaa  
1 5 10 15

His Cys Cys Ser Gly Xaa Cys Leu Phe Val Cys Ala  
20 25

<110> P02  
<111> 140  
<112> ENA  
<113> *Onchus arenatus*

<120>  
<121> CDS  
<122> 7 .. (246)

<210>  
<211> misc\_feature  
<212> 1 .. (340)  
<223> n. may be any nucleotide

<400> P02  
ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg ctg ttc ttg 48  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
1 5 10

acc gcc tgg aca ttc gtc acg gct gac tcc ata cgt gca ctg gag gat 96  
Thr Ala Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp

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15          20          25          30
ttt ttt gcg aag gca cgt gac gaa atg gaa aac agc gga gct tct cca      144
Phe Phe Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro
          35          40          45

ttg aac gag aga gac tgg cga cct gta ggt caa tat tgt ggc ata ccc      192
Leu Asn Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro
          50          55          60

tat aag cac aac tgg cga tgc tgc agt cag ctt tgt gca att atc tgt      240
Tyr Lys His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys
          65          70          75

ggt tcc taaccctctt gatcctactc tctgaagacc tccgggattc aacatccaaa      296
Val Ser
          80

taaaacgaca tcccgatnaa aaaaaaangaa aaaaaaaaaa aaaa      340

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<210> 303
<211> 80
<212> PRT
<213> Conus arenatus

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<220>
<221> misc_feature
<222> (1)..(340)
<223> n may be any nucleotide

```

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<400> 313

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Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1          5          10          15

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Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp Phe Phe
          20          25          30

```

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Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro Leu Asn
          35          40          45

```

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Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro Tyr Lys
          50          55          60

```

```

His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
          65          70          75          80

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<210> 304
<211> 31
<212> PRT
<213> Conus arenatus

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<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residues 4 and 12 may be Pro or hydroxy-Pro; Xaa at residu
es 8 and 13 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, C-
sulpho-Tyr or O-phospho-Tyr; Xaa at residue 17 may be Trp or brom

```

o-Trp

&lt;400&gt; 304

Asp Cys Arg Xaa Val Gly Gln Xaa Cys Gly Ile Xaa Xaa Lys His Asn  
 1 5 10 15

Xaa Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser  
 20 25 30

&lt;210&gt; 335

&lt;211&gt; 281

&lt;212&gt; DNA

&lt;213&gt; Conus arenatus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 71..(334)

&lt;400&gt; 305

gggttc atg aat ctg acg tgt gtg gtg atc gtt gtt gtg ctg ttc ttg 48  
 Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu  
 1 5 10

acc gcc tgg aca ttc gtc aag gct gat gac tcc ata aat gga ttg gag 96  
 Phe Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu  
 15 20 25 30

aat ctt ttt cag aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144  
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser  
 35 40 45

aaa ttg aac gag agg tgc ctt gaa aag ggt gta ctt tgt gat ccg agt 192  
 Lys Leu Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser  
 50 55 60

gct gca aac tgc tgt agt ggc gaa tgc gtt tta gtc tgc etc 234  
 Ala Gly Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu  
 65 70 75

taaaaactacc gtgatgtctt ctactcccat ctgtgctacc cctcgag 281

&lt;210&gt; 306

&lt;211&gt; 76

&lt;212&gt; FET

&lt;213&gt; Conus arenatus

&lt;400&gt; 306

Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu  
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser Ala Gly

50

55

60

Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu  
61 70 75

<210> 307  
<211> 25  
<212> PET  
<213> Conus arenatus

<220>  
<221> SITE  
<222> (1) ..(25)  
<223> Xaa at residues 3 and 19 may be Glu or gamma-carboxy-Glu; Xaa at  
residue 10 may be Pro or hydroxy-Pro

<400> 3 7

Cys Leu Xaa Lys Gly Val Leu Cys Asp Xaa Ser Ala Gly Asn Cys Cys  
1 5 10 15

Ser Gly Xaa Cys Val Leu Val Cys Leu  
20 25

<210> 303  
<211> 247  
<212> DNA  
<213> Conus arenatus

<220>  
<221> CDS  
<222> (1) ..(240)

<400> 3 3

ggatcc atg aaa atg acg tgc atg gtg atc gtt act gtg ttg ttc ttg 48  
Met Lys Leu Thr Cys Met Val Ile Val Thr Val Leu Phe Leu  
1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gaa ttg gag 96  
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu  
15 20 25 30

aat ctt ttt atg aag gca tat cac gaa atg aac tcc gaa gcc tct aaa 144  
Asn Leu Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys  
35 40 45

ttg gac aag aaa gag tgc gtt gct ggt agt cac ttt tgt ggt ttt ccg 192  
Leu Asp Lys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro  
50 55 60

aaa att gga ggg cca tgc tgc agt ggc tgg tgc ttt ttc gtc tgc ttg 240  
Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu  
65 70 75

taaacctgac gtgatgtatt ctactcccat ctgtgctacc cctcgag 288

<210> 310  
<211> 28  
<212> PRT  
<213> Conus arenatus

&lt;400&gt; 309

Met Lys Leu Thr Cys Met Val Ile Val Thr Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu Asn Leu  
20 25 30

Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys Leu Asp  
35 40 45

Lys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro Lys Ile  
50 55 60

Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu  
65 70 75

&lt;210&gt; 310

&lt;211&gt; 23

&lt;212&gt; FFT

&lt;213&gt; Cinus arenatus

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)...(28)

<223> Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residues  
12 and 17 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Trp  
or bromo-Trp

&lt;400&gt; 310

Xaa Cys Val Ala Gly Ser His Phe Cys Gly Phe Xaa Lys Ile Gly Gly  
1 5 10 15

Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu  
20 25

&lt;210&gt; 311

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Cinus tessulatus

&lt;220&gt;

&lt;221&gt; DIS

&lt;222&gt; (7)...(243)

&lt;400&gt; 311

ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg atg ttc ttg 48  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu  
1 5 10

acc gcc tgg aca ttc atc acg gct gat gac tcc ata aat gga ctg gag 96  
Thr Ala Trp Thr Phe Ile Thr Ala Asn Asp Ser Ile Asn Gly Leu Glu  
15 20 25 30

gat aga ggc ata tgg ggg gaa cct ttg tgg aag gca cgt gac gaa atg 144  
Asp Arg Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met

	35	40	45	
aac ccc gaa gtc tct aaa cgg gat tgc tgg cct caa tat tgg ttt tgt				192
Asn Pro Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys				
	50	55	60	
ggc cta cag agg gga tgc tgc cca ggg act act tgc ttc ttc ctt tgc				240
Gly Leu Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys				
	65	70	75	
ttt tagtgatctc ttgactccc ttctgtgcta cctggcttga cctttgattg				293
Phe				
gcgcgtgcac ttcactgggtt ataaacccct ctgttccctcc tctctggacg cttcggggtg				353
tccagcatcc aaataaagcg acgtccccc aaataaaaaa aaataaaa				400

<210> 312  
 <211> 79  
 <212> ERT  
 <213> Conus tessulatus

<400> 312

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu Thr Ala			
1	5	10	15

Trp Thr Phe Ile Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asp Arg			
	20	25	30

Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met Asn Pro			
	35	40	45

Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys Gly Leu			
	50	55	60

Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys Phe			
	65	70	75

<110> 313  
 <111> 26  
 <112> ERT  
 <113> Conus tessulatus

<120>  
 <121> SITE  
 <222> (1)...(26)  
 <223> Xaa at residues 3 and 7 may be Trp or bromo-Trp; Xaa at residues 4 and 17 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or C-prosper-Tyr

<400> 313

Asp Cys Xaa Xaa Gln Xaa Xaa Phe Cys Gly Leu Gln Arg Gly Cys Cys			
1	5	10	15

Xaa Gly Thr Thr Cys Phe Phe Leu Cys Phe  
20 25

<210> 314  
<211> 419  
<212> DNA  
<213> *Conus tessulatus*

<220>  
<221> CDS  
<222> (7)..(249)

<400> 314  
ggatgc arg aaa ctg acg tgc gtg gtg gtc gtt gct gtg ctg ttc ttg 48  
Met Lys Leu Thr Cys Val Val Val Val Ala Val Leu Phe Leu  
1 5 10  
aac gcc tgg aga ttc gcc acg gct gtt gac tcc aaa cat gca ctg gcg 96  
Asn Ala Trp Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala  
15 20 25 30  
aaa ctt ttt atg aag gca cgt gac gaa atg tat aac ccc gat gcc act 144  
Lys Leu Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr  
35 40 45  
aaa tgc gac gat aag aga tgg tgc gct tta gat ggt gaa ctt tgt atc 192  
Lys Leu Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile  
50 55 60  
ata cgg gtc att ggg tcc ata ttt tgc tgc cat ggc ata tgt atg atc 240  
Ile Pro Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile  
65 70 75  
aac tgc gtc tagttgaact gccgtgatgt cttctactcc cctctgtgct 289  
Tyr Cys Val  
80  
aaccttggtt tgatctttga ttgccctgtg cccctcactg attatgaatc cctctgatcc 349  
tactctctga agaccctttg gggccaaca tccaaataaa ggcacatccc aaaaaaaaaa 409  
aaaaaaaaa 419

<210> 315  
<211> 81  
<212> EST  
<213> *Conus tessulatus*

<400> 315

Met Lys Leu Thr Cys Val Val Val Val Ala Val Leu Phe Leu Asn Ala  
1 5 10 15  
Trp Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala Lys Leu  
20 25 30  
Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr Lys Leu  
35 40 45



Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile Ile Pro  
50 55 60

Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile Tyr Cys  
65 70 75 80

Val

<210> 316  
<211> 29  
<212> PPT  
<213> *Conus tessulatus*

<220>  
<221> SITE  
<222> (1)..(29)  
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be  
e Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Pro or hydro  
xy-Pro; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, d  
i-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 316

Xaa Cys Ala Leu Asp Gly Xaa Leu Cys Ile Ile Xaa Val Ile Gly Ser  
5 10 15  
Ile Phe Cys Cys His Gly Ile Cys Met Ile Xaa Cys Val  
20 25

<410> 317  
<411> 408  
<412> DNA  
<413> *Conus imperialis*

<220>  
<221> CDS  
<222> (17)..(240)

<400> 317  
ggatcc atg aaa ctg acg tgc gtg gtg ttc gtt gct gtg ccg ttc ttg 18  
Met Lys Leu Thr Cys Val Val Phe Val Ala Val Pro Phe Leu  
1 5 10

acc gcc tgc gta ttc atc acg gct gat gac tcc aga aat gga atc gag 36  
Thr Ala Ser Val Phe Ile Thr Ala Asp Asp Ser Arg Asn Gly Ile Glu  
15 20 25 30

aac ctt cct ccg atg aga cgt cac gaa atg aag aac ccc aaa gac tct 114  
Asn Leu Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser  
35 40 45

aaa ttg aac aag aga cag tgc cgt gta gaa ggt gaa att tgt ggc atg 12  
Lys Leu Asn Lys Arg Gln Cys Arg Val Glu Gly Glu Ile Cys Gly Met  
50 55 60

ctg ttt gaa gca caa tgc tgc gat ggc tgg tgc ttt ttc gtc tgc atg 240  
Leu Phe Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met  
65 70 75

taaaaactgcc gtgatgtctt ctactctcct ctgtgctacc tgcctgata ttgattggc 300  
 tcgcgccttt cattgggttat gaacccctct gatcctactc tetggaggcc tcaggggtcc 360  
 agcatctaaa taaagcgaca tcacaatcaa aaaaaaaaaa aaaaaaaa 403

<210> 318  
 <211> 78  
 <212> PFT  
 <213> Conus imperialis

<400> 318

Met Lys Leu Thr Cys Val Val Phe Val Ala Val Pro Phe Leu Thr Ala  
 1 5 10 15

Ser Val Phe Ile Thr Ala Asp Asp Ser Arg Asn Gly Ile Glu Asn Leu  
 20 25 30

Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Gln Cys Arg Val Glu Gly Glu Ile Cys Gly Met Leu Phe  
 50 55 60

Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met  
 65 70 75

<210> 318  
 <211> 27  
 <212> PFT  
 <213> Conus imperialis

<220>  
 <221> SITE  
 <222> (1)..(27)  
 <223> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 5, 7 and  
 14 may be Glu or gamma-carboxy-Glu; Xaa at residue 21 may be Trp  
 or bromo-Trp

<400> 319

Xaa Cys Arg Val Xaa Gly Xaa Ile Cys Gly Met Leu Phe Xaa Ala Gln  
 1 5 10 15

Cys Cys Asp Gly Xaa Cys Phe Phe Val Cys Met  
 20 25

<210> 320  
 <211> 281  
 <212> DNA  
 <213> Conus characteristicus

<210>  
 <221> CDS  
 <222> (7)..(234)

<400> 320  
 ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg ctg ttc ttg 48  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
 1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag 96  
 Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu  
 15 20 25 30

aat ctt ttt cgg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144  
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser  
 35 40 45

aaa ttg aac aag agg tgc gtt gac cct ggt gaa ttt tgt ggt ccg gga 192  
 Lys Leu Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly  
 50 55 60

ttt gga gat tgc tgc act ggc ttc tgc ctt tta gtc tgc atc 234  
 Phe Gly Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile  
 65 70 75

taaaactgac gtgatgtctt ctactcccat ctgtgctacc cctcgag 281

<210> 311  
 <211> 70  
 <212> PRT  
 <213> Conus characteristic

<400> 311

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly Phe Gly  
 50 55 60

Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile  
 65 70 75

<210> 322  
 <211> 15  
 <212> PRT  
 <213> Conus characteristic

<220>  
 <221> SITE  
 <222> 1) .. (25)  
 <223> Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residue  
 6 may be Glu or gamma-carboxy-Glu

<400> 322

Cys Val Asp Xaa Gly Xaa Phe Cys Gly Xaa Gly Phe Gly Asp Cys Cys  
 1 5 10 15

Thr Gly Phe Cys Leu Leu Val Cys Ile  
 20 25

<210> 323  
 <211> 287  
 <212> DNA  
 <213> Conus miliaris

<220>  
 <221> CDS  
 <222> (7) .. (240)

<400> 323  
 gattac atg aaa ctg aag tgc gtg gtg atc gtt gct gtg ttg ttc ttg 48  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
 1 5 10

acc gcc tgg aca ttc gtc atg gct gat gac tcc aga aat gat ttg gag 96  
 Thr Ala Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu  
 15 20 25 30

aat att ttt ctg aag gca cgt cat gaa atg aag aac ccc gaa gct tct 144  
 Asn Leu Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser  
 35 40 45

aaa ttg aac aag aga tgc ctt cca aat ggt gta att tgt gat ctg gga 192  
 Lys Leu Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly  
 50 55 60

tct gca cca tac tgc tgc agt ggc tgg tgc ggc atc gtc gtc tgc atc 240  
 Ser Pro Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile  
 65 70 75

taaaactgac gtcattgtctt ctactcccat ctgtgtctacc cctcgag 287

<210> 324  
 <211> 78  
 <212> FET  
 <213> Conus miliaris

<400> 324

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu Asn Leu  
 20 25 30

Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly Ser Pro  
 50 55 60

Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile

65

70

75

<210> 325  
 <211> 27  
 <212> PET  
 <213> Conus miliaris

<220>  
 <221> SITE  
 <222> (1)..(27)  
 <223> Xaa at residues 3, 13 and 14 may be Pro or hydroxy-Pro; Xaa at residue 15 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulphat-Tyr or O-phospho-Tyr; Xaa at residue 20 may be Trp or bromo-Trp

<400> 315

Cys Leu Xaa Asn Gly Val Leu Cys Asp Leu Gly Ser Xaa Xaa Xaa Cys  
 1 5 10 15

Cys Ser Gly Xaa Cys Ala Ile Val Val Cys Ile  
 20 25

<210> 326  
 <211> 28  
 <212> CNA  
 <213> Conus atlanticus

<220>  
 <221> SITE  
 <222> (1)..(240)

<400> 316  
 ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 48  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
 1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac tcc ata aat ggg ttg gag 96  
 Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu  
 15 20 25 30

aat ctt ttt ccg aag gca cgt cac gaa atg agg aaa ccc gaa gcc tct 144  
 Asn Leu Phe Pro Lys Ala Arg His Glu Met Arg Lys Pro Glu Ala Ser  
 35 40 45

aga tcc aga ggg agg tgc cgt cct cgt ggt atg ttc tgt ggc ttt ccg 192  
 Arg Ser Arg Gly Arg Cys Arg Pro Arg Gly Met Phe Cys Gly Phe Pro  
 50 55 60

aac cct gga cca tac tgc tgc aat ggc tgg tgc ttt ttc gtc tgc atc 240  
 Lys Pro Gly Pro Tyr Cys Cys Asn Gly Trp Cys Phe Phe Val Cys Ile  
 65 70 75

taaaactccc gtgatgtgtt ctactcccat ctgtgctacc cctggag 287

<21> 317  
 <211> 28  
 <212> ERI  
 <213> Conus atlanticus

<400> 317

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Pro Lys Ala Arg His Glu Met Arg Lys Pro Glu Ala Ser Arg Ser  
35 40 45

Arg Gly Arg Cys Arg Pro Arg Gly Met Phe Cys Gly Phe Pro Lys Pro  
50 55 60

Gly Pro Tyr Cys Cys Asn Gly Trp Cys Phe Phe Val Cys Ile  
65 70 75

<210> 338  
<211> 2"  
<212> PRT  
<213> *Conus atlanticus*

<220>  
<221> SITE  
<222> 11... (27)  
<223> Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa at residue 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or bromo-Trp

<400> 328

Cys Arg Xaa Arg Gly Met Phe Cys Gly Phe Xaa Lys Xaa Gly Xaa Xaa  
1 5 10 15

Cys Lys Asn Gly Xaa Cys Phe Phe Val Cys Ile  
20 25

<210> 329  
<211> 234  
<212> DNA  
<213> *Conus lividus*

<220>  
<221> CDS  
<222> 17... (237)

<400> 329

ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc atg 15  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gaa ttc gaa 11  
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu  
15 20 25 30

aat ctt ttt tgc aag gca cat cac gaa atg aag aac ccc gaa gcc tct 144  
Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser  
35 40 45

gaa caa aac tgc tgc tat acc tat tgc ttr att gta gtc tgc cta 237  
Glu Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu  
64 70 75

42104 330  
 42114 77  
 42124 PFT  
 42134 *Conus lividus*

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
5 10 15

Asp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
38 40 45

Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln  
50 55 60

Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu  
65 70 75

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<210> 331
<211> 26
<212> PST
<213> Citrus lividus

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<220>
<221> SITE
<222> 10..(26)
<223> Xaa at residue 2 may be Pro or hydroxy-Pro; Xaa at residues 6 and
12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 ma
y be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
O-phospho-Tyr

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<400> 331

Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys  
5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu  
20 25

<210>	532
<211>	281
<212>	DNA

<213> Conus pulicarius

<220>

<221> CDS

<222> (7)..(234)

<400> 332

ggatcc atg aaa ctg acg tgc atg gtg atc gtt gct gtg ctg ttc ttg 48  
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu  
1 5 10

acc gcc tgg aca ttc gtc aag gct gat gac tcc aga aat gga ttg gag 96  
Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu  
15 20 25 30

aat ctt ttt cgg aag gca cgt cac gaa atg aag aac tcc aaa gcc tct 144  
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser  
35 40 45

aaa tta aac aag agg tgc gtt gaa gat ggt gat ttt tgt ggt cgg gga 192  
Lys Leu Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly  
50 55 60

tat gaa gag tgc tcc agt ggc ttc tgc ctt tac gtc tgc atc 234  
Tyr Glu Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile  
65 70 75

taaaactgac gtgatgtctt ctactcccat ctgtgtacac cctcgag 281

<210> 333

<211> 76

<212> PPT

<213> Conus pulicarius

<400> 333

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser Lys Leu  
35 40 45

Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly Tyr Glu  
50 55 60

Glu Lys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile  
65 70 75

<210> 334

<211> 23

<212> PPT

<213> Conus pulicarius

<220>

<221> SITE



<222> (1)..(25)

<223> Xaa at residues 3, 13 and 14 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Pro or hydroxy-Pro; Xaa at residues 12 and 22 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or C-phospho-Tyr

<400> 334

Cys Val Xaa Asp Gly Asp Phe Cys Gly Xaa Gly Xaa Xaa Xaa Cys Cys  
1 5 10 15

Ser Gly Phe Cys Leu Xaa Val Cys Ile  
20 25

<210> 335

<211> 393

<212> LNA

<213> Conus generalis

<220>

<221> CDS

<222> (1)..(249)

<400> 335  
ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg cta ttc ttg 48  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac acc aga tat aaa ctg gag 96  
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu  
15 20 25 30

aat cct ttt ctg aag gca cgc aac gaa ctg cag aaa cac gaa gcc tct 144  
Asn Pro Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser  
35 40 45

caa ctg aac gag aga ggc tgc ctt gac cca ggt tac ttc tgt ggg acg 192  
Gln Leu Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr  
50 55 60

ccg ttt ctt gga gca tac tgc tgc ggt gcc att tgc ctt att gtc tgc 240  
Pro Phe Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys  
65 70 75

ata gaa acg taaaggcttg atgtcttcta ctcccatctg tgetacccct agag 293  
Ile Glu Thr  
80

<210> 336

<211> 81

<212> PRT

<213> Conus generalis

<400> 336

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Ile Leu Thr Ser  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu Asn Pro  
20 25 30

Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser Gln Leu  
35 40 45

Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr Pro Phe  
50 55 60

Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Glu  
65 70 75 80

Thr

<210> 337  
<211> 30  
<212> FFT  
<213> *Conus generalis*

<220>  
<221> SITE  
<222> (1)..(30)  
<223> Xaa at residues 5 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 337

Gly Lys Leu Asp Xaa Gly Xaa Phe Cys Gly Thr Xaa Phe Leu Gly Ala  
1 5 10 15

Xaa Lys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Xaa Thr  
20 25 30

<210> 338  
<211> 400  
<212> TNA  
<213> *Conus episcopatus*

<220>  
<221> TIS  
<222> (7)..(234)

<400> 338

ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 48  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 46  
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly  
15 20 25 30

aat ctt ttt tgg aat gta cat cac gaa atg aag aac ctg gaa gac tct 44  
Asn Leu Phe Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser  
35 40 45

aaa ttg gac aag aag tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt 192  
Lys Leu Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu  
50 55 60

tat tca gac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta 234  
 Tyr Ser Asp Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu  
       65                    70                    75

taaaaactaac gtgaagtttt ctactccctt ctgtgctacc tggcttgatc ttgattggc 294  
 ctgtggtgtt caatgggttat gaacccctct gatcctaact tctgaagacc tctgggggtcc 354  
 aacatccaaa taaagcgaca tcacaaaaaaaa aaaaaaaaaa aaaaaa 400

<210> 339  
 <211> 76  
 <212> PRT  
 <213> Conus episcopatus

<400> 339

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1                    5                    10                    15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu  
       20                    25                    30

Phe Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser Lys Leu  
       35                    40                    45

Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser  
       50                    55                    60

Asp Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu  
       65                    70                    75

<210> 340  
 <211> 85  
 <212> PRT  
 <213> Conus episcopatus

<220>  
 <221> SITE  
 <222> 1)...(25)  
 <223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residues  
       12 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s  
       ulpho-Tyr or O-phospho-Tyr

<400> 340

Cys Leu Gly Phe Gly Xaa Ala Cys Leu Met Leu Xaa Ser Asp Cys Cys  
 1                    5                    10                    15

Ser Xaa Cys Val Ala Leu Val Cys Leu  
       20                    25

<210> 341  
 <211> 404  
 <212> DNA  
 <213> Conus episcopatus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(240)

&lt;400&gt; 341

ggatcc atg aaa ctg acg tgc gtg gtg atc att gct gtg ctg ttc ttg 48  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu  
 1 5 10

acc gcc tgg aca ttc gtc atg gct gat gac ccc aga gat gaa ccg gag 96  
 Thr Ala Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu  
 15 20 25 30

gca cgt gac gaa atg aac ccc gca gcc tct aaa ttg aac gag aga ggc 144  
 Ala Arg Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly  
 35 40 45

tgc ctt gca gtt gat tat ttt tgc gcc ata ccg ttt gtg agc aac ggc 192  
 Cys Leu Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly  
 50 55 60

cta tgc tgc agt gcc aat tgt gtt ttt gtc tgc aca ccc caa ggc aag 240  
 Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys  
 65 70 75

taaaactgca gtgacgtctt ctactccct ctgtgctacc tggttgatc ttgattggc 300

ggtgcactt cactgggtat gaacccctct gatccctactc tetgaagacc tetgggggtcc 360

aaatccaaa taaagcgaca tcccaaaaaa aaaaaaaaaa aaaa 404

&lt;21&gt; 342

&lt;211&gt; 78

&lt;212&gt; PPT

<213> *Conus episcopatus*

&lt;400&gt; 342

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg  
 20 25 30

Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu  
 35 40 45

Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly Leu Cys  
 50 55 60

Lys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys  
 65 70 75

&lt;21&gt; 342

&lt;211&gt; 31

&lt;212&gt; PPT

<213> *Conus episcopatus*

<220>  
 <221> SITE  
 <222> (1)..(31)  
 <223> Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydroxy-Pro

<400> 343

Gly Cys Leu Ala Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Ser Asn  
 1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln  
 20 25 30

<210> 344

<211> EST

<212> DNA

<213> Conus achatinus

<220>

<221> CDS

<222> (1..171)

<400> 344

cgatctctg tctccatct attattattc gtgtccaaac tgtgttaaatt attcaagtct 60

atctctctgt ttgtgtctaa cagg ttg aga tgg tgc att cct aga ggt gat 111  
 Leu Arg Trp Cys Ile Pro Arg Gly Asp  
 1 5

ctt tgt ttc ccc tgg gat cgc ata caa tgc tgc agt ggc aag tgc aca 159  
 Leu Cys Phe Pro Ser Asp Arg Ile Gln Cys Cys Ser Gly Lys Cys Thr  
 10 15 20 25

ttc gtc tgc atg taaaactgcc gtgatgtctt ctctccct c 202  
 Phe Val Cys Met

<210> 345

<211> EST

<212> EST

<213> Conus achatinus

<400> 345

Leu Arg Trp Cys Ile Pro Arg Gly Asp Leu Cys Phe Pro Ser Asp Arg  
 1 5 10 15

Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
 20 25

<210> 346

<211> 27

<212> EST

<213> Conus achatinus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 11 may be Pro or hydroxy-Pro

<400> 346

Xaa Cys Ile Xaa Arg Gly Asp Leu Cys Phe Xaa Ser Asp Arg Ile Gln  
1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
20 25

<210> 347

<211> 252

<212> DNA

<213> *Genus achatinus*

<220>

<221> CDS

<222> (15)..(171)

<400> 347

cgatctctg tctctctctt tcattcattc gctgccaaac tgtattaaat attcgaatct 60

ctctctctct ttgtgtctga caga ttg aga ggg tgc gtt cct agt ggt gaa 111  
Leu Arg Gly Cys Val Pro Ser Gly Glu  
1 5

att tgt tac ttc atg gat cac ata gga tgc tgc agt ggc aag tgc aca 159  
Ile Cys Tyr Phe Met Asp His Ile Gly Cys Cys Ser Gly Lys Cys Thr  
10 15 20 25

ttc gtc tgc atg taaaactgcc gtgatgtctt ctctctccat c 202  
Phe Val Lys Met

<210> 348

<211> 23

<212> FRT

<213> *Genus achatinus*

<400> 348

Leu Arg Gly Cys Val Pro Ser Gly Glu Ile Cys Tyr Phe Met Asp His  
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
20 25

<210> 349

<211> 17

<212> FRT

<213> *Genus achatinus*

<220>

<221> CITE

<222> (1)..(27)

<223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 349

Gly Cys Val Xaa Ser Gly Xaa Ile Cys Xaa Phe Met Asp His Ile Gly  
 1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
 20 25

&lt;210&gt; 350

&lt;211&gt; 264

&lt;212&gt; DNA

&lt;213&gt; Conus bullatus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 1)..(234)

&lt;400&gt; 350

arg aaa atg aag tgc gtg atg atc gtt act gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala  
 1 5 10 15

agg aca ttc gtc aag gct gat gac tcc aca tat gga ttg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Thr Tyr Gly Leu Lys Asn Leu  
 20 25 30

ttg atg aac gga cgt cat gaa atg atg aac ccc gaa gcc cct aaa ttg 144  
 Leu Pro Asn Gly Arg His Glu Met Met Asn Pro Glu Ala Pro Lys Leu  
 35 40 45

aac aag aaa gat gaa tgc tct gct cct ggt gca ttt tgt cac atc agg 192  
 Asn Lys Lys Asp Glu Cys Ser Ala Pro Gly Ala Phe Cys Leu Ile Arg  
 50 55 60

aca gga atc tgc tgc agc gag ttc tgc ttc ttt gcg tgt ttt 234  
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Phe Ala Cys Phe  
 65 70 75

tagtgacggt tgatgtcttc tactcccttc 264

&lt;210&gt; 351

&lt;211&gt; 75

&lt;212&gt; EST

&lt;213&gt; Conus bullatus

&lt;400&gt; 351

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Thr Tyr Gly Leu Lys Asn Leu  
 20 25 30

Leu Pro Asn Gly Arg His Glu Met Met Asn Pro Glu Ala Ile Lys Leu  
 35 40 45

Asn Lys Lys Asp Glu Cys Ser Ala Pro Gly Ala Phe Cys Leu Ile Arg  
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Phe Ala Cys Phe  
65 70 75

<210> 352

<211> 27

<212> PRT

<213> Conus bullatus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residues 2 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residues 6 and 14 may be Pro or hydroxy-Pro

<400> 352

Asp Xaa Cys Ser Ala Xaa Gly Ala Phe Cys Leu Ile Arg Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Phe Ala Cys Phe  
20 25

<210> 353

<211> 276

<212> DNA

<213> Conus bullatus

<220>

<221> CDS

<222> (1)..(246)

<400> 353

atg aaa ctg acg tgc gtg atg atc gtt act gtg ctg ttc ttg acc gcc 48  
Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga gac gat ccg gat agt gca 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala  
20 25 30

gaa gga tgg gag aaa ctt ttc tgg gag gca cgt gac gaa atg aag aac 144  
Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn  
35 40 45

cgc aaa gac ttt gaa ttg aga ggg tgc ctt cct agg tgg gaa ttt tgt 192  
Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys  
50 55 60

ccc atc ttt aaa aaa aac gat tgc tgc agt ggc ata tgc ata agc atc 240  
Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile  
65 70 75 80

tgc ttg taaaactcgg tgatgtcttc tcttccatc 276  
Cys Leu

<210> 354

<211> 82

<212> PRT

<213> Conus bullatus



&lt;400&gt; 354

Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala  
 20 25 30

Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn  
 35 40 45

Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys  
 50 55 60

Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile  
 65 70 75 80

Cys Leu

&lt;210&gt; 355

&lt;211&gt; 27

&lt;212&gt; PBT

&lt;213&gt; Conus bullatus

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(27)

<223> Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residue  
 6 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma  
 -carboxy-Glu

&lt;400&gt; 355

Gly Cys Leu Xaa Arg Xaa Xaa Phe Cys Xaa Ile Phe Lys Lys Asn Asp  
 1 5 10 15

Cys Cys Ser Gly Ile Cys Ile Ser Ile Cys Leu  
 20 25

&lt;210&gt; 356

&lt;211&gt; 268

&lt;212&gt; LNA

&lt;213&gt; Conus striolatus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(237)

&lt;400&gt; 356

atg aaa ctg acg tgc atg atg att gtt get gtg atg ttc ttg acc gcc  
 Met Lys Leu Thr Cys Met Met Ile Val A'. Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg ata ttt gta atg get gat gac tcc aga aat gga ttg gag aat ctt  
 Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu

48

96

20	25	30	
cct cag act aca cgt cac gaa atg aag aac ccc gaa gcc tct aaa ttg			144
Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu			
35	40	45	
aac cag aca gac tgc ctt gct aaa gac gct ttc tgt gcc tgg ccg ata			192
Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile			
50	55	60	
ctt gga cca ctg tgc tgc agt cgc ttg tgc tta tac gtc tgc atg			237
Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met			
65	70	75	
taaaactgcc gtgatgtctt ctactccct c			268

<210> 357  
 <211> 79  
 <212> PRT  
 <213> Conus striolatus

<400> 357

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala		
1	5	10 15

Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu		
20	25	30

Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu		
35	40	45

Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile		
50	55	60

Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met		
65	70	75

<210> 358  
 <211> 28  
 <212> PRT  
 <213> Conus striolatus

<220>

<221> SITE

<222> (1)..(28)

<223> Xaa at residue 11 may be Trp or bromo-Trp; Xaa at residues 12 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tyr, 125-1-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

<400> 358

Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa		
1	5	10 15

Leu Cys Cys Ser Arg Leu Cys Leu Xaa Val Cys Met		
20	25	

<210> 359  
 <211> 266  
 <212> DNA  
 <213> Consensus

<220>  
 <221> CDS  
 <222> (1) .. (246)

<400> 359  
 atg aaa atg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
 20 25 30  
 tct cag aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tgg 144  
 Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser  
 35 40 45  
 aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac 192  
 Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn  
 50 55 60  
 gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240  
 Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr  
 65 70 75 80  
 ttt tgg tgaatgtcttc tcttcccttc 266  
 Phe Ser

<210> 360  
 <211> 82  
 <212> PRT  
 <213> Consensus

<400> 360

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
 20 25 30  
 Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser  
 35 40 45  
 Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn  
 50 55 60  
 Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr  
 65 70 75 80  
 Phe Ser

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<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-
      Iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be
      Glu or gamma-carboxy-Glu

```

Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu  
5 10 15  
Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser  
20 25 30

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<220 .
<221 . CDS
<222 . (1) .. (252)
```

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<21 > 363
<211> 84
<21. > PRT
<213> Conus consors
```

&lt;400&gt; 363

Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Thr  
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu  
 20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45

Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg  
 50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
 65 70 75 80

Val Asp Ser Gly

&lt;210&gt; 364

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Conus consors

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(32)

<223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty  
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or  
 hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;  
 Xaa at residue 25 may be Trp or bromo-Trp

&lt;400&gt; 364

Asp Gly Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu  
 1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser  
 20 25 30

&lt;210&gt; 365

&lt;211&gt; 205

&lt;212&gt; DNA

&lt;213&gt; Conus circumcissus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (83)..(175)

&lt;400&gt; 365

agatccatct gtccatccat ctatttattt attgctgtgt aaactttatt aaattatcaa

gtctctcttt ctgttttgtt ct aac aga ttg a t agt ttt att att agt ggt  
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly  
 1 5 10

60

111

gat ctt tgt ttc ccc tgc gat cac ata caa tgc tgc aat gcc aag tgc 160  
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys  
 15 20 25

gca ttc gtc tgc ttg taaaaactgcc gtgatgtctt ctattccctc 205  
 Ala Phe Val Cys Leu  
 30

<210> 366  
 <211> 31  
 <212> FFT  
 <213> Conus circumcissus

<400> 366

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser  
 1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu  
 20 25 30

<210> 367  
 <211> 26  
 <212> FFT  
 <213> Conus circumcissus

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

<400> 367

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys  
 1 5 10 15

Cys Asn Ala Lys Cys Ala Phe Val Cys Leu  
 20 25

<210> 368  
 <211> 206  
 <212> DNA  
 <213> Conus circumcissus

<220>  
 <221> CDS  
 <222> (83)..(175)

<400> 368  
 cgaaccatct gtccatccat ctattcattc attcgtgtgc aaactgtatt aaatattcaa 60

gtctctcttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112  
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly  
 1 5 10

gat ctt tgt ttc ccc tgc gat cac ata caa tgc tgc agt gcc aag tgc 160  
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys  
 15 20 25

gca ttc gtc tgc ttg taaaaactgcc gtgatgtctt ctattccctc 206

Ala Phe Val Cys Leu  
30

<210> 369  
<211> 31  
<212> PRT  
<213> Conus circumcissus  
  
<400> 369

Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser  
1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu  
20 25 30

<210> 370  
<211> 27  
<212> PRT  
<213> Conus circumcissus  
  
<220>  
<221> SITE  
<222> (1)..(27)  
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1  
1 may be Pro or hydroxy-Pro

<400> 370

Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln  
1 5 10 15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu  
20 25

<210> 371  
<211> 206  
<212> DNA  
<213> Conus circumcissus

<220>  
<221> CDS  
<222> (83)..(175)

<400> 371  
cgatccatct gtccatccat ctattccattc attcgtgtgc aaactgtatt aaatattcaa 60  
gtctctcttt ctgttttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112  
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly  
1 5 10  
gat ctt tgt ttc ccc tgc gat cac ata caa tgc tgc agt gcc aag tgc 160  
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys  
15 20 25  
gca ttc gtc tgc ttg taaaactgcc gtgatgtatt ctctccct c 206  
Ala Phe Val Cys Leu  
30

<210> 372  
 <211> 31  
 <212> PPT  
 <213> Conus circumcissus

<400> 372

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser  
 1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu  
 20 25 30

<210> 373  
 <211> 26  
 <212> PPT  
 <213> Conus circumcissus

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

<400> 373

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys  
 1 5 10 15

Cys Ser Ala Lys Cys Ala Phe Val Cys Leu  
 20 25

<210> 374  
 <211> 206  
 <212> DNA  
 <213> Conus circumcissus

<220>  
 <221> CDS  
 <222> (33)..(175)

<400> 374  
 cgaaccatct gtccatccat ctattcattc attcgtctgc aaactgtatt aaatattcaa 60  
 gtctctcttt ctgttttgtt ct aac aga ttg agt agg tgc att cct agt ggt 112  
 Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly  
 1 5 10  
 gat ctt tgt ttc ccc tgg gat cag ata caa tgc tgc aat gcc gag tgc 160  
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Glu Cys  
 15 20 25  
 gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctctctccct c 216  
 Ala Phe Val Cys Leu  
 30

<210> 375  
 <211> 31  
 <212> PPT  
 <213> Conus circumcissus



&lt;400&gt; 375

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser  
 1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Glu Cys Ala Phe Val Cys Leu  
 20 25 30

&lt;210&gt; 376

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Conus circumcissus

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(26)

&lt;223&gt; Xaa at residues 3 and 10 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu

&lt;400&gt; 376

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys  
 1 5 10 15

Cys Asn Ala Xaa Cys Ala Phe Val Cys Leu  
 20 25

&lt;210&gt; 377

&lt;211&gt; 206

&lt;212&gt; DNA

&lt;213&gt; Conus circumcissus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (83)..(175)

&lt;400&gt; 377

cgatccatct gtcacatccat ctatccatcc attcgcgtgac aaactgtatt aaatattcaa 60

gtctctcttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112  
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly  
 1 5 10

gat ctt tgt ttc ccc tgg gat cac ata cga tgc tgc agt gcc aag tgc 160  
 Asp Leu Cys Phe Pro Ser Asp His Ile Arg Cys Cys Ser Ala Lys Cys  
 15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcttcccat c 206  
 Ala Phe Val Cys Leu  
 30

&lt;210&gt; 378

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Conus circumcissus

&lt;400&gt; 377

Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser  
 1 5 10 15

Asp His Ile Arg Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu  
                   20                  25                  30

<210> 379

<211> 27

<212> PRT

<213> Conus circumcissus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1  
           1 may be Pro or hydroxy-Pro

<400> 379

Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Arg  
   1                  5                  10                  15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu  
                   20                  25

<210> 380

<211> 206

<212> DNA

<213> Conus circumcissus

<220>

<221> CDS

<222> (83)..(175)

<400> 330  
 cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa 60

gtctctcttt ctgttttgtt ct aac aga ttg agt agg tgc att cct agt ggt 112  
                                   Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly  
                                   1                  5                  10

gat ctt tgt ttc ccc tgg gat cac ata caa tgc tgc aat gcc aag tgc 160  
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys  
                   15                  20                  25

gca ttc gcc tgc ttg taaaactgcc gtgatgtatt ctattccctc 206  
 Ala Phe Ala Cys Leu  
                   30

<210> 381

<211> 31

<212> PRT

<213> Conus circumcissus

<400> 381

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser  
   1                  5                  10                  15

Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu  
                   20                  25                  30

<210> 232  
 <211> 25  
 <212> PRT  
 <213> Conus circumcissus

<220>  
 <221> SITE  
 <222> (1)..(26)  
 <223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

<400> 382

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys  
 1 5 10 15  
 Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu  
 20 25

<210> 383  
 <211> 206  
 <212> CNA  
 <213> Conus circumcissus

<220>  
 <221> CTS  
 <222> (3)..(175)

<400> 383  
 cgcacccat t gtcacccat ctattccatc attcgctgcc aaactgtatt aaatattcaa 60  
 gtctctctt t ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112  
 Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly  
 1 5 10  
 gat ctt tgt ttc ccc tgg gat cac ata caa tgc tgc aat gcc aag tgc 160  
 Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys  
 15 20 25  
 gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctactccct c 206  
 Ala Phe Val Cys Leu  
 30

<210> 384  
 <211> 31  
 <212> PRT  
 <213> Conus circumcissus

<400> 384

Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser  
 1 5 10 15  
 Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu  
 20 25 30

<210> 385  
 <211> 27  
 <212> PRT

<213> Conus circumcissus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 11 may be Pro or hydroxy-Pro

<400> 385

Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln  
1 5 10 15

Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu  
20 25

<210> 386

<211> 200

<212> ENA

<213> Conus circumcissus

<220>

<221> CDS

<222> (77)..(169)

<400> 386

cgagctcttg cctctctctt ttattatttg ctgcctaactg tattaatat tcaagtctct 60

ctttctgttt gtgtct aac aga ttg agt tgg tgc att cct act ggt gat ctt 112  
Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu  
1 5 10

tgt ttc ccc tgg gat cac ata caa tgc tgc agt ggc aag tgc aca ttc 160  
Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe  
15 20 25

gtc tgc atg taaaactgcc gtgatgtctt cctctccct c 200  
Val Cys Met  
30

<210> 387

<211> 31

<212> PRT

<213> Conus circumcissus

<400> 387

Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu Cys Phe Pro Ser  
1 5 10 15

Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
20 25 30

<210> 388

<211> 37

<212> PRT

<213> Conus circumcissus

<220>

<221> SITE

<222> (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 11 may be Pro or hydroxy-Pro

<400> 388

Xaa Cys Ile Xaa Thr Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln  
 1 5 10 15  
 Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met  
 20 25

<210> 389

<211> 266

<212> DNA

<213> *Conus monachus*

<220>

<221> CDS

<222> (1)..(246)

<400> 389

atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
 20 25 30

tct ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tgg 144  
 Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser  
 35 40 45

aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac 192  
 Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn  
 50 55 60

gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240  
 Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr  
 65 70 75 80

ttt tgg tgatgtcttc tctctccctc 266  
 Phe Ser

<210> 390

<211> 82

<212> FRT

<213> *Conus monachus*

<400> 390

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
 20 25 30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser

35

40

45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn  
 50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr  
 65 70 75 80

Phe Ser

<210> 391  
 <211> 31  
 <212> PRT  
 <213> Conus monachus

<220>  
 <221> SITE  
 <222> (1)..(31)  
 <223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

&lt;400&gt; 391

Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu  
 1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser  
 20 25 30

<210> 392  
 <211> 277  
 <212> DNA  
 <213> Conus stercusmuscarum

<220>  
 <221> IDS  
 <222> (1)..(246)

<400> 392  
 atg aaa ctg acg tgc atg atg atc gtt gct gtg ctc ttc ttg acc gcc 48  
 Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

tgg aca ttc gtc aca gct gat gac tcc ata aat gga ccc gag aat aga 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg  
 20 25 30

cga ata tgg gag aaa ctt ttg ttg aag gca cgt gac gaa atg aag aac 144  
 Arg Ile Trp Glu Lys Leu Leu Leu Lys Ala Arg Asp Glu Met Lys Asn  
 35 40 45

acc gaa gcc tct caa ttg aga tgg tgc att cct agt ggt gaa ctt tgt 192  
 Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys  
 50 55 60

ttc cgc tgc gat cac ata caa tgc tgc agt gcc aag tgc gca ttc gtc 240  
 Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val

65

70

75

80

tgc ttg taaaactacc gtgatgtctt cctctcccat c  
Cys Leu

277

&lt;210&gt; 393

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Conus stercusmuscarum

&lt;400&gt; 393

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg  
20 25 30

Arg Ile Trp Glu Lys Leu Leu Leu Lys Ala Arg Asp Glu Met Lys Asn  
35 40 45

Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys  
50 55 60

Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val  
65 70 75 80

Cys Leu

&lt;210&gt; 394

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus stercusmuscarum

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(27)

<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be  
Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy  
-Glu

&lt;400&gt; 394

Xaa Cys Ile Xaa Ser Gly Xaa Leu Cys Pro Arg Ser Asp His Ile Glu  
1 5 10 15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu  
20 25

&lt;210&gt; 395

&lt;211&gt; 260

&lt;212&gt; INA

&lt;213&gt; Conus stercusmuscarum

<220>  
 <221> CDS  
 <222> (1)..(246)

<400> 395  
 atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg atc gcc 48  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala  
 1 5 10 15  
 tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg aag aat ctt 96  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu  
 20 25 30  
 ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 aac aag aga gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cgt 192  
 Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg  
 50 55 60  
 cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240  
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
 65 70 75 80  
 att gat tga tgc ttc ttt ccc ctc 266  
 Ile Asp

<210> 396  
 <211> 82  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 396  
 Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala  
 1 5 10 15  
 Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu  
 20 25 30  
 Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu  
 35 40 45  
 Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg  
 50 55 60  
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe  
 65 70 75 80  
 Ile Asp

<210> 397  
 <211> 31  
 <212> PRT



<213> Conus stercusmuscarum

<220>

<221> SITE

<222> (1) .. (31)

<223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or bromo-Trp

<400> 397

Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp  
20 25 30

<210> 398

<211> 266

<212> ENA

<213> Conus striolatus

<220>

<221> CDS

<222> (1) .. (234)

<400> 398

atg aaa ctg acg tgc ata atg acc gtt gct gtg ctg ttc ttg acc gct 48  
Met Lys Leu Thr Cys Ile Met Thr Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

agg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96  
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
20 25 30

ctt ctg aag aca cgt cac gaa gtg gaa aac ccc aaa gcc tct agg tgg 144  
Leu Leu Lys Thr Arg His Glu Val Glu Asn Pro Lys Ala Ser Arg Ser  
35 40 45

ggc ggt agg tgc cgt cct ggt ggt acg gtt tgt ggc ttt cag aaa cct 192  
Gly Gly Arg Cys Arg Pro Gly Gly Thr Val Cys Gly Phe Pro Lys Pro  
50 55 60

gga cca aac tgc tgc agt ggc tgg tgc ttt ttt gtc tgc gcc 234  
Gly Pro Tyr Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Ala  
65 70 75

taaacctgcc gtgatgttt ctcctcccat c 265

<21> 399

<211> 71

<212> F&T

<213> Conus striolatus

<400> 399

Met Lys Leu Thr Cys Ile Met Thr Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu  
20 25 30

Leu Leu Lys Thr Arg His Glu Val Glu Asn Pro Lys Ala Ser Arg Ser  
35 40 45

Gly Gly Arg Cys Arg Pro Gly Gly Thr Val Cys Gly Phe Pro Lys Pro  
50 55 60

Gly Iro Tyr Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Ala  
65 70 75

<210> 400  
<211> 27  
<212> PFT  
<213> Conus striolatus

<220>  
<221> SITE  
<222> (1) .. (27)  
<223> Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa at residue 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or bromo-Trp

<400> 400

Cys Arg Xaa Gly Gly Thr Val Cys Gly Phe Xaa Lys Xaa Gly Xaa Xaa  
1 5 10 15

Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Ala  
20 25

<210> 401  
<211> 272  
<212> DNA  
<213> Conus striolatus

<220>  
<221> CDS  
<222> (1) .. (243)

<400> 401  
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 18  
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 24  
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 30  
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 36  
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
50 55 60

ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240  
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly

65

70

75

80

ggg taactgcccgt gatgtcttct attcccctc  
Gly

272

&lt;210&gt; 403

&lt;211&gt; 81

&lt;212&gt; PFT

&lt;213&gt; Conus striolatus

&lt;400&gt; 402

Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His  
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu  
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys  
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly  
65 70 75 80

Gly

&lt;210&gt; 403

&lt;211&gt; 29

&lt;212&gt; PFT

&lt;213&gt; Conus striolatus

&lt;220&gt;

&lt;221&gt; SIE

&lt;222&gt; (1)..(29)

<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at  
residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s  
ulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may b  
e Pro or hydroxy-Pro

&lt;400&gt; 403

Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu  
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly  
20 25

&lt;210&gt; 4 4

&lt;211&gt; 205

&lt;212&gt; DNA

&lt;213&gt; Conus striolatus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(246)

&lt;400&gt; 404

atg	aaa	ctg	acg	tgt	ctg	atg	gct	ggt	gct	ctg	ctg	ttc	ttg	acc	gcc	48
Met	Lys	Leu	Thr	Cys	Leu	Met	Ala	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala	
1				5				10					15			

egg	aca	ttc	gtc	acg	gct	gat	gac	tcc	aga	aat	gga	ttg	gag	aat	ctt	96
Arg	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Glu	Asn	Leu	
			20					25					30			

tct	cag	aag	gca	cgt	cac	gaa	atg	aag	aac	ccc	gaa	gcc	tct	aaa	tcg	144
Ser	Pro	Lys	Ala	Arg	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Ser	
		35					40					45				

aac	aag	aga	tat	gag	tgc	tat	tct	act	ggt	aca	ttt	tgt	ggc	atc	aac	192
Asn	Lys	Arg	Tyr	Glu	Cys	Tyr	Ser	Thr	Gly	Thr	Phe	Cys	Gly	Ile	Asn	
	50					55					60					

gga	gga	ctc	tgc	tgc	agc	aac	ctt	tgc	tta	ttt	ttc	gtg	tgc	tta	aca	240
Gly	Gly	Leu	Cys	Cys	Ser	Asn	Leu	Cys	Leu	Phe	Phe	Val	Cys	Leu	Thr	
65					70				75					80		

ttt	tgg	tgatgtcttc	tatcccttc													265
Phe	Ser															

&lt;210&gt; 405

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Conus striolatus

&lt;400&gt; 405

Met	Lys	Leu	Thr	Cys	Leu	Met	Ala	Val	Ala	Val	Leu	Phe	Leu	Thr	Ala
1				5				10					15		

Arg	Thr	Phe	Val	Thr	Ala	Asp	Asp	Ser	Arg	Asn	Gly	Leu	Glu	Asn	Leu
			20					25					30		

Ser	Pro	Lys	Ala	Arg	His	Glu	Met	Lys	Asn	Pro	Glu	Ala	Ser	Lys	Ser
		35					40					45			

Asn	Lys	Arg	Tyr	Glu	Cys	Tyr	Ser	Thr	Gly	Thr	Phe	Cys	Gly	Ile	Asn
	50					55					60				

Gly	Gly	Leu	Cys	Cys	Ser	Asn	Leu	Cys	Leu	Phe	Phe	Val	Cys	Leu	Thr
65					70				75					80	

Phe Ser

&lt;210&gt; 406

&lt;211&gt; 31

<212> PRT  
<213> *Conus striolatus*

<220>  
<221> SITE  
<222> (1)..(31)  
<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 406

Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu  
1 5 10 15  
Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser  
20 25 30

<210> 407  
<211> 237  
<212> DNA  
<213> *Conus striolatus*

<220>  
<221> CDS  
<222> (1)..(231)

<400> 407  
atg aaa ctg acg tgt atg gtg atc gtc gcc gtg ctg ctc ctg acg acc 48  
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Thr  
1 5 10 15  
tgt cat ctc atc aca gct gat gac tcc aga ggt acg cag aag cat cgt 96  
Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30  
tcc ctg agg tgg act acc aaa gtc tcc aag tgg act agc tgc atg aaa 144  
Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys  
35 40 45  
gcc ggg tct tat tgc gtc gct act acg aga atc tgc tgc ggt tat tgc 192  
Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys  
50 55 60  
gct tat ttc ggc aaa ata tgt att ggc tat ccc aaa aac tgatctctcc 241  
Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn  
65 70 75  
cttactgtgc tctatcttt ttgtgctgat gtctttctct cccctc 287

<210> 408  
<211> 77  
<212> PRT  
<213> *Conus striolatus*

<400> 408

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Thr  
1 5 10 15  
Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg

20

25

30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys  
 35 40 45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys  
 50 55 60

Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn  
 65 70 75

<210> 409

<211> 35

<212> PRT

<213> Conus striolatus

<220>

<221> SITE

<222> (1)..(35)

<223> Xaa at residues 10, 21, 24 and 32 may be Tyr, 125-I-Tyr, mono-iod  
 o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue  
 33 may be Pro or hydroxy-Pro

<400> 409

Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg  
 1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Gly Xaa  
 20 25 30

Xaa Lys Asn  
 35